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200
↙

Sequence	Length	Code
VLAEAMSQV (SEQ ID NO:70)	9	A
ILKEPVHGV (SEQ ID NO:71)	9	B
TLNFPISPI (SEQ ID NO:72)	9	C
SLLNATDIAV (SEQ ID NO:73)	10	D
QMAVFIHNFK (SEQ ID NO:74)	10	E
VTVYYGVPVWK (SEQ ID NO:75)	11	F
FPVRPQVPL (SEQ ID NO:76)	9	G
YPLASLRSLF (SEQ ID NO:77)	10	H
VIYQYMDDLY (SEQ ID NO:78)	10	I
IYQEPFKNL (SEQ ID NO:79)	9	J
IWGCSGKLI (SEQ ID NO:80)	9	K

202

AA	C+1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

204

Motif Specification

XXXX(FY)XX(LIMV) (SEQ ID NO:370)
 XXXX(FY)XXX(LIMV) (SEQ ID NO:371)
 XXXXNXXX(LIMV) (SEQ ID NO:372)
 XXXXNXXXX(LIMV) (SEQ ID NO:373)
 X(LM)XXXXXXXV (SEQ ID NO:374)
 X(LM)XXXXXXXV (SEQ ID NO:375)
 X(LMVT)XXXXXXX(KRY) (SEQ ID NO:376)
 X(LMVT)XXXXXXX(KRY) (SEQ ID NO:377)
 XPXXXXXXX(LIMVF) (SEQ ID NO:378)
 XPXXXXXXX(LIMVF) (SEQ ID NO:379)

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FIG. 11A



Replacement Sheet

Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

204

The following 10 motif specifications will be used to search for junctionals.

Count Motif Specification

1	XXXX(FY)XX(LIMV) (SEQ ID NO:370)
2	XXXX(FY)XXX(LIMV) (SEQ ID NO:371)
3	XXXXNXXX(LIMV) (SEQ ID NO:372)
4	XXXXNXXXX(LIMV) (SEQ ID NO:373)
5	X(LM)XXXXXXV (SEQ ID NO:374)
6	X(LM)XXXXXXXV (SEQ ID NO:375)
7	X(LMVT)XXXXXX(KRY) (SEQ ID NO:376)
8	X(LMVT)XXXXXX(KRY) (SEQ ID NO:377)
9	XPXXXXXX(LIMVF) (SEQ ID NO:378)
10	XPXXXXXX(LIMVF) (SEQ ID NO:379)

206

Code	Peptide	Length
A	VLAEMSQV (SEQ ID NO:70)	9
B	ILKEPVHGV (SEQ ID NO:71)	9
C	TLNFPISPI (SEQ ID NO:72)	9
D	SLLNATDIAV (SEQ ID NO:73)	10
E	QMAVFIHNFK (SEQ ID NO:74)	10
F	VTVYYGVPVWK (SEQ ID NO:75)	11
G	FPVRPQVPL (SEQ ID NO:76)	9
H	YPLASLRSLF (SEQ ID NO:77)	10
I	VIYQYMDDL Y (SEQ ID NO:78)	10
J	IYQEPFKNL (SEQ ID NO:79)	9
K	IWGCSGKLI (SEQ ID NO:80)	9

202

MaxInsertions = 4 (208)

FIG. 13A

Replacement Sheet



Protein	Sequence	Restriction	(SEQ ID NO:)
HIV gag 386	VLAEAMSQV	HLA-A2	143
HIV gag 271	MTNNPPIPV	HLA-A2	144
HIV pol 774	MASDFNLPPV	HLA-A2	145
HIV pol 448	KLVGKLNWA	HLA-A2	146
HIV pol 163	LVGPTPVNI	HLA-A2	147
HIV pol 498	ILKEPVHGV	HLA-A2	148
HIV pol 879	KAACWWAGI	HLA-A2	149
HIV pol 132	KMIGGIGGFI	HLA-A2	150
HIV pol 772	RAMASDFNL	HLA-A2	151
HIV pol 183	TLNFPISPI	HLA-A2	152
HIV env 134	KLTPLCVTL	HLA-A2	153
HIV env 651	LLQLTVWGI	HLA-A2	154
HIV env 163	SLLNATDIAV	HLA-A2	155
HIV nef 221	LTFGWCFKL	HLA-A2	156
HIV vpr 59	AIIRILQQL	HLA-A2	157
HIV vpr 62	RILQQLFI	HLA-A2	158
HIV pol 929	QMAVFIHNFK	HLA-A3	159
HIV pol 722	KVYLAWVPAHK	HLA-A3	160
HIV pol 971	KIQNFRVYYR	HLA-A3	161
HIV pol 347	AIFQSSMTK	HLA-A3	162
HIV pol 98	VTIKIGGQLK	HLA-A3	163
HIV env 61	TTLFCASDAK	HLA-A3	164
HIV env 47	VTVYYGVPVWK	HLA-A3	165
HIV nef 100	QVPLRPMTYK	HLA-A3	166
HIV vif 7	VMIVWQVDR	HLA-A3	167
HIV gag 162	QMVHQAISPR	HLA-A3	168
HIV gag 545	YPLASLRSLF	HLA-B7	169
HIV gag 237	HPVHAGPIA	HLA-B7	170
HIV pol 186	FPISPIETV	HLA-B7	171
HIV pol 893	IPYNPQSQGVV	HLA-B7	172
HIV env 259	IPIHYCAPA	HLA-B7	173
HIV env 250	CPKVSFEPI	HLA-B7	174
HIV nef 94	FPVRPQVPL	HLA-B7	175
HIV rev 75	VPLQLPPL	HLA-B7	176
HIV pol 684	EVNIVTDSQY	HLA-A1	177
HIV gag 317	FRDYVDRFY	HLA-A1	178
HIV pol 368	VIYQYMDDL	HLA-A1	179
HIV pol 295	VTVLDVGDAY	HLA-A1	180
HIV pol 533	IYQEPFKNL	HLA-A24	181
HIV pol 244	PYNTPVFAI	HLA-A24	182
HIV pol 530	TYQIQEPF	HLA-A24	183
HIV pol 597	YWQATWIPEW	HLA-A24	184
HIV env 681	IWGCSGKLI	HLA-A24	185
HIV env 671	RYLKDQQLL	HLA-A24	186

FIG. 19A

Replacement Sheet



Protein	Sequence	Restriction	(SEQ ID NO:)
HIV env 55	VWKEATTTLF	HLA-A24	187
HIV vpr 46	IYETYGDTW	HLA-A24	188
HIV vpr 14	PYNEWTLEL	HLA-A24	189
HIV gag 298	KRWIILGLNKIVRMY	HLA-DR	190
HIV pol 596	WEFVNTPLVLKLYWYQ	HLA-DR	191
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR	192
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR	193
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR	194
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR	195
HIV env 729	QHLLQLTVWGIKQLQ	HLA-DR	196
HIV gag 171	QGQMVHQAI SPRTL N	HLA-DR	197
HIV pol 335	SPAIFQSSMTKILEP	HLA-DR	198
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR	199
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR	200
HIV pol 758	HSNWRAMASDFNLPP	HLA-DR	201
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR	202
HIV vpu 31	YRKILRQRKIDRLID	HLA-DR3	203
HIV pol 874	WAGIKQEF GIPYNPQ	HLA-DR3	204
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3	205
HIV pol 619	AETFYVDGAANRETK	HLA-DR3	206
HIV pol 989	GAVVIQD NSDIKVVP	HLA-DR3	207
HCV NS4 1812	LLFNILGGWV	HLA-A2	208
HCV NS1/E2 728	FLLLADARV	HLA-A2	209
HCV NS4 1590	YLVAYQATV	HLA-A2	210
HCV NS5 2611	RLIVFPDLGV	HLA-A2	211
HCV CORE 132	DLMGYIPLV	HLA-A2	212
HCV NS4 1920	WMNRLIAFA	HLA-A2	213
HCV NS4 1666	VLVGGVLAA	HLA-A2	214
HCV NS4 1769	HMWNFISGI	HLA-A2	215
HCV NS4 1851	ILAGYGAGV	HLA-A2	216
HCV CORE 35	YLLPRRG PRL	HLA-A2	217
HCV NS1/E2 726	LLFLLLADA	HLA-A2	218
HCV LORF 1131	YLVTRHADV	HLA-A2	219
HCV CORE 51	KT SERSQPR	HLA-A3	220
HCV CORE 43	RLGVRATRK	HLA-A3	221
HCV ENV1 290	QLFTFSRR	HLA-A3	222
HCV NS1/E2 632	RMVVG GVEHR	HLA-A3	223
HCV NS3 1396	LIFCHSKKK	HLA-A3	224
HCV NS4 1863	GVAGALVAFK	HLA-A3	225
HCV NS4 1864	VAGALVAFK	HLA-A3	226
HCV NS3 1262	LGFGAYMSK	HLA-A3	227
HCV Core 169	LPGCSFSIF	HLA-B7	228
HCV NS5 2922	LSAFSLHSY	HLA-A1	229
HCV NS3 1128	CTCGSSDLY	HLA-A1	230
HCV NS5 2180	LTDPSHITA	HLA-A1	231

FIG. 19B

Replacement Sheet



Protein	Sequence	Restriction	(SEQ ID NO:)
HCV Core 126	LTCGFADLMGY	HLA-A1	232
HCV NS3 1305	LADGGCSGGAY	HLA-A1	233
HCV NS4 1765	FWAKHMWNF	HLA-A24	234
HCV NS5 2875	RMILMTHFF	HLA-A24	235
HCV NS5 2639	VMGSSYGF	HLA-A24	236
HCV NS4 1765	FWAKHMWNFI	HLA-A24	237
P. falciparum SSP2-230	FMKAVCDEV	HLA-A2	238
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2	239
P. falciparum CSP-7	ILSVSSFLFV	HLA-A2	240
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3	241
P. falciparum LSA1-105	GVSENIFLK	HLA-A3	242
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3	243
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7	244
P. falciparum LSA1-1663	LPSENERGY	HLA-A1	245
P. falciparum EXP1-73	KYKLATSVL	HLA-A24	246
P. falciparum CSP-12	SFLFVEALF	HLA-A24	247
P. falciparum LSA1-10	YFILVNLLI	HLA-A24	248
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2	249
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2	250
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2	251
P. falciparum SSP2-523	LACAGLAYK	HLA-A3	252
P. falciparum EXP1-10	ALFFIIFNK	HLA-A3	253
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3	254
P. falciparum SSP2-126	LPYGRTNL	HLA-B7	255
P. falciparum CSP-15	FVEALFQEY	HLA-A1	256
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1	257
P. falciparum LSA1-9	FYFILVNLL	HLA-A24	258
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24	259
P. falciparum CSP-394	GLIMVLSFL	HLA-A2	260
P. falciparum EXP1-2	KILSVFFLA	HLA-A2	261
P. falciparum CSP-344	VTGNGIQVR	HLA-A3	262
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3	263
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1	264
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24	265
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24	266
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24	267
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24	268
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24	269
P. falciparum LSA1-5	LYISFYFI	HLA-A24	270
P. falciparum CSP-2	MRKLAILSVSSFLFV	HLA-DR	271
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR	272
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR	273
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR	274
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3	275
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3	276

FIG. 19C

Replacement Sheet



Protein	Sequence	Restriction	(SEQ ID NO:)
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR	277
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR	278
P. falciparum SSP2-527	GLAYKFVVPGAATPY	HLA-DR	279
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR	280
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR	281
P. falciparum LSA1-16	LLIFHINGKIIKNSE	HLA-DR	282
P. falciparum LSA1-94	QTNFKSLLRNLGVSE	HLA-DR	283
HBV core 18	FLPSDFFPSV	HLA-A2	284
HBV env 183	FLLTRILTI	HLA-A2	285
HBV env 335	WLSLLVPFV	HLA-A2	286
HBV pol 455	GLSRYVARL	HLA-A2	287
HBV pol 538	YMDDVVLGV	HLA-A2/A1	288
HBV pol 773	ILRGTSFVYV	HLA-A2	289
HBV pol 562	FLLSLGIHL	HLA-A2	290
HBV pol 642	ALMPYACI	HLA-A2	291
HBV env 338	GLSPTVWLSV	HLA-A2	292
HBV core 141	STLPETTIVRR	HLA-A3	293
HBV pol 149	HTLWKAGILYK	HLA-A3/A1	294
HBV pol 150	TLWKAGILYK	HLA-A3	295
HBV pol 388	LVVDFSQFSR	HLA-A3	296
HBV pol 47	NVSIPWTHK	HLA-A3	297
HBV pol 531	SAICSVVRR	HLA-A3	298
HBV pol 629	KVGNTGLY	HLA-A3/A1	299
HBV pol 665	QAFTFSPTYK	HLA-A3	300
HBV core 19	LPDFFPSV	HLA-B7	301
HBV env 313	IPSSWAF	HLA-B7	302
HBV pol 354	TPARVTGGVF	HLA-B7	303
TB	RMSRVTTFTV	HLA-A2	304
TB	ALVLLMLPVV	HLA-A2	305
TB	LMIGTAAAVV	HLA-A2	306
TB	ALVLLMLPV	HLA-A2	307
TB	GLMTAVYLV	HLA-A2	308
TB	MALLRLPV	HLA-A2	309
TB	RMFAANLGV	HLA-A2	310
TB	SLYFGGICV	HLA-A2	311
TB	RLPLVLPV	HLA-A2	312
TB	RLMIGTAAA	HLA-A2	313
TB	FVVALIPLV	HLA-A2	314
TB	MTYAAPLFV	HLA-A2	315
TB	AMALLRLPLV	HLA-A2	316
p53 139	KLCPVQLWV	HLA-A2	317
CEA 687	ATVGIMIGV	HLA-A2	318
CEA 691	IMIGHLVGV	HLA-A2	319
Her2/neu 689	RLLQETELV	HLA-A2	320
MAGE3 112	KVAEIVHFL	HLA-A2	321

FIG. 19D



Protein	Sequence	Restriction	(SEQ ID NO:)
Her2/neu 369	KVFGSLAFV	HLA-A2	322
CEA 605	YLSGANLNV	HLA-A2	323
MAGE2 157	YLQLVFGIEV	HLA-A2	324
Her2/neu 665	VVLGVVFGI	HLA-A2	325
p53 149	SMPPPGTRV	HLA-A2	326
PAP.21.T2	LTFFWLDRSV	HLA-A2	327
PAP.112	TLMSAMTNL	HLA-A2	328
PAP.284	IMYSAHDTTV	HLA-A2	329
PSM.288.V10	GLPSIPVHPV	HLA-A2	330
PSM.441	LLQERGVAYI	HLA-A2	331
PSM.469L2	LLYSLVHNL	HLA-A2	332
PSM.663	MMNDQLMFL	HLA-A2	333
PSA.3.V11	FLTLSVTWIGV	HLA-A2	334
PSA.143.V8	ALGTTCYV	HLA-A2	335
PSA.161	FLTPKKLQCV	HLA-A2	336
HuK2.4.L2	LLLSIALSV	HLA-A2	337
HuK2.53.V11	VLVHPQWVLTV	HLA-A2	338
HuK2.165	FLRPRSLQCV	HLA-A2	339
HuK2.216.V11	PLVCNGVLQGV	HLA-A2	340

FIG. 19E

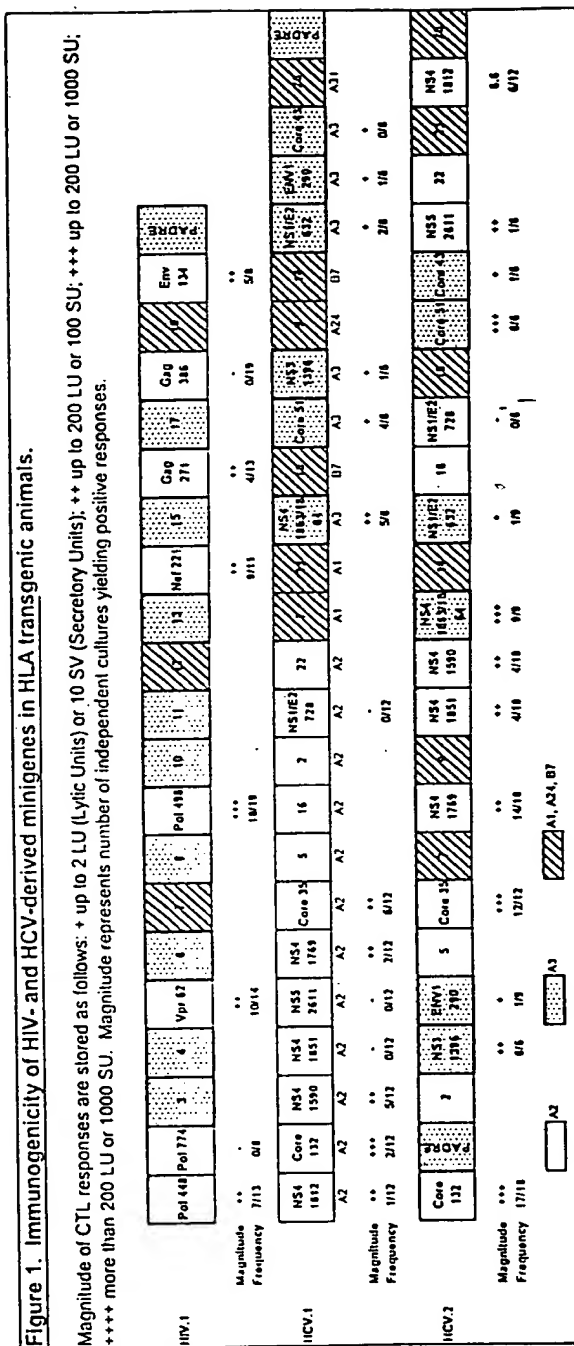
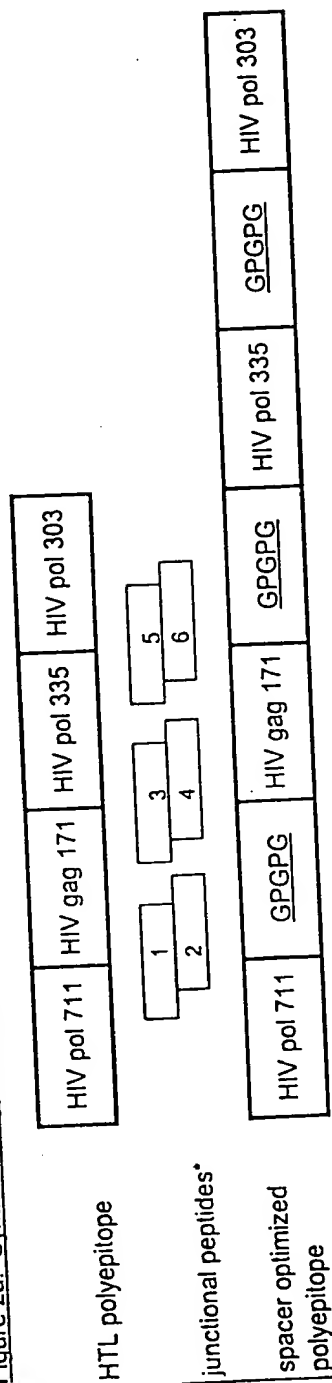


FIGURE 1

Figure 2a. Synthetic polypeptides encoding HIV-derived HTL epitopes



* junctional peptides comprise either 10 amino acids from the N-terminal epitope and 5 amino acids from the C-terminal epitope or 5 amino acids from the N-terminal epitope and 10 amino acids from the C-terminal epitope.

Figure 2b. Proliferative responses to synthetic polypeptides encoding HIV-derived HTL

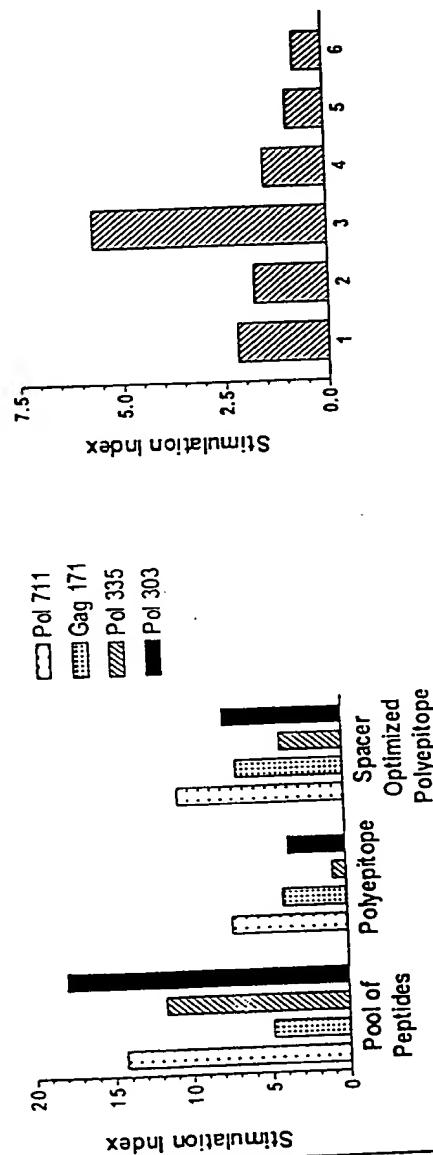
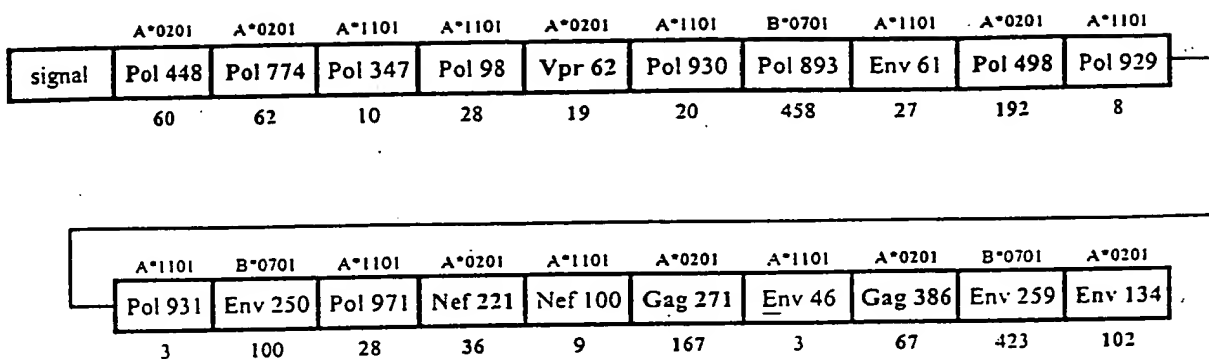


FIGURE 2

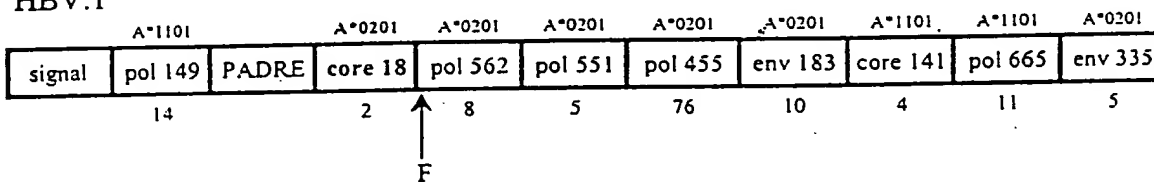


a: HIV-FT

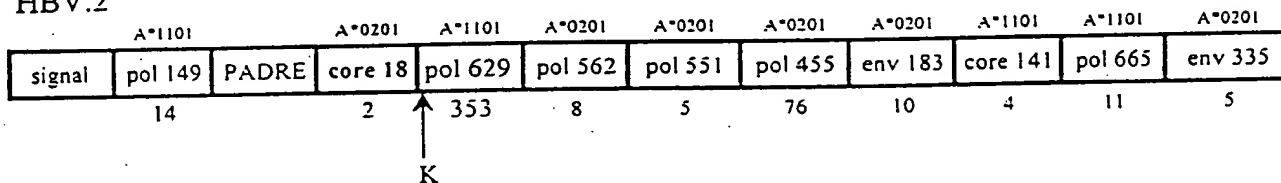


b: HBV-specific multiepitope constructs

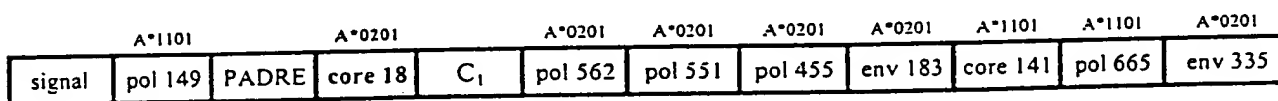
HBV.1



HBV.2



HBV.1X



C₁= either W, Y, L, K, R, C, N or G

FIGURE 3

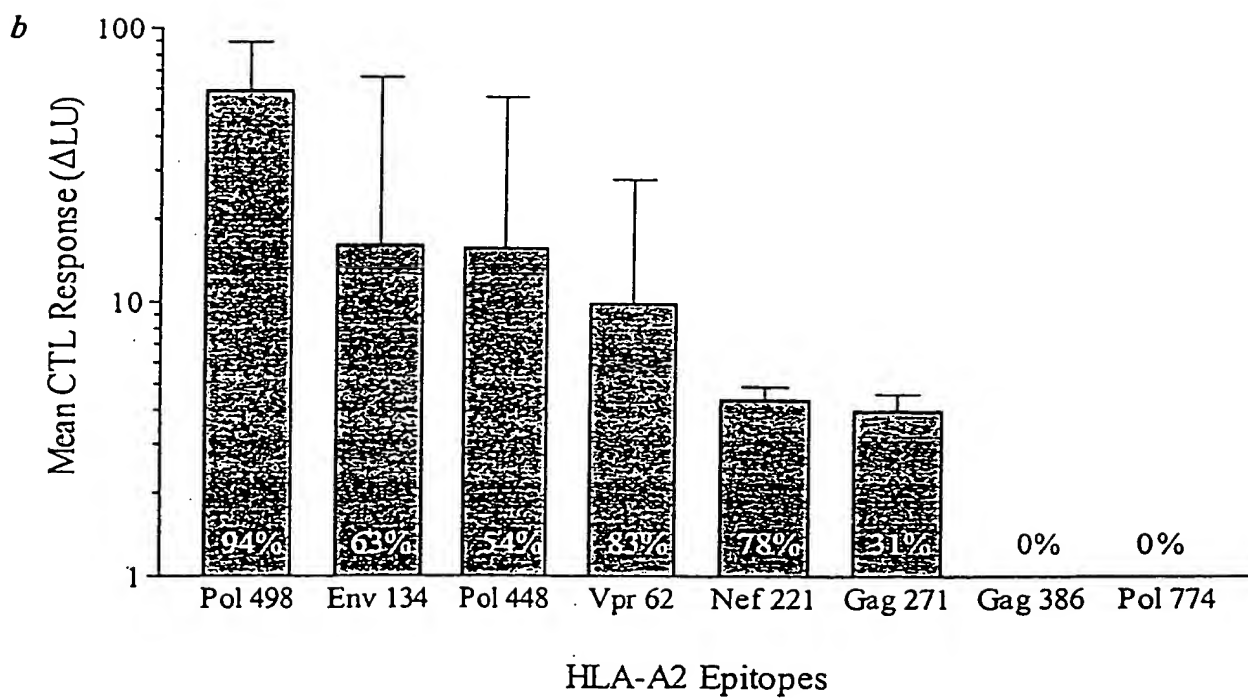
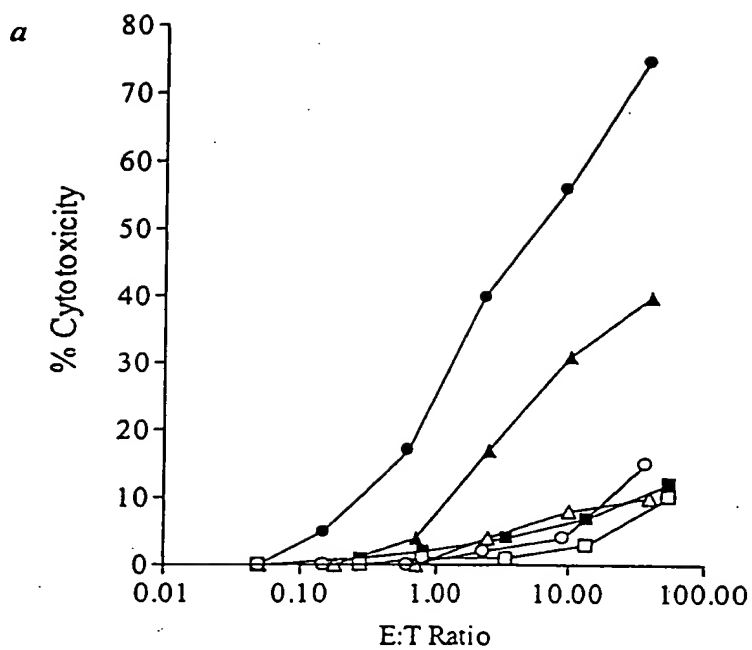


FIGURE 4

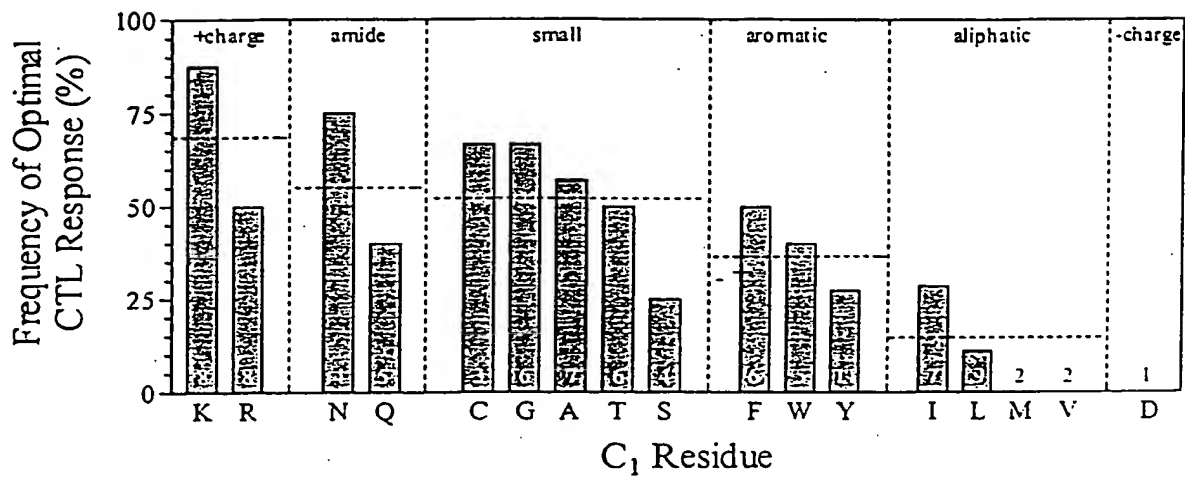
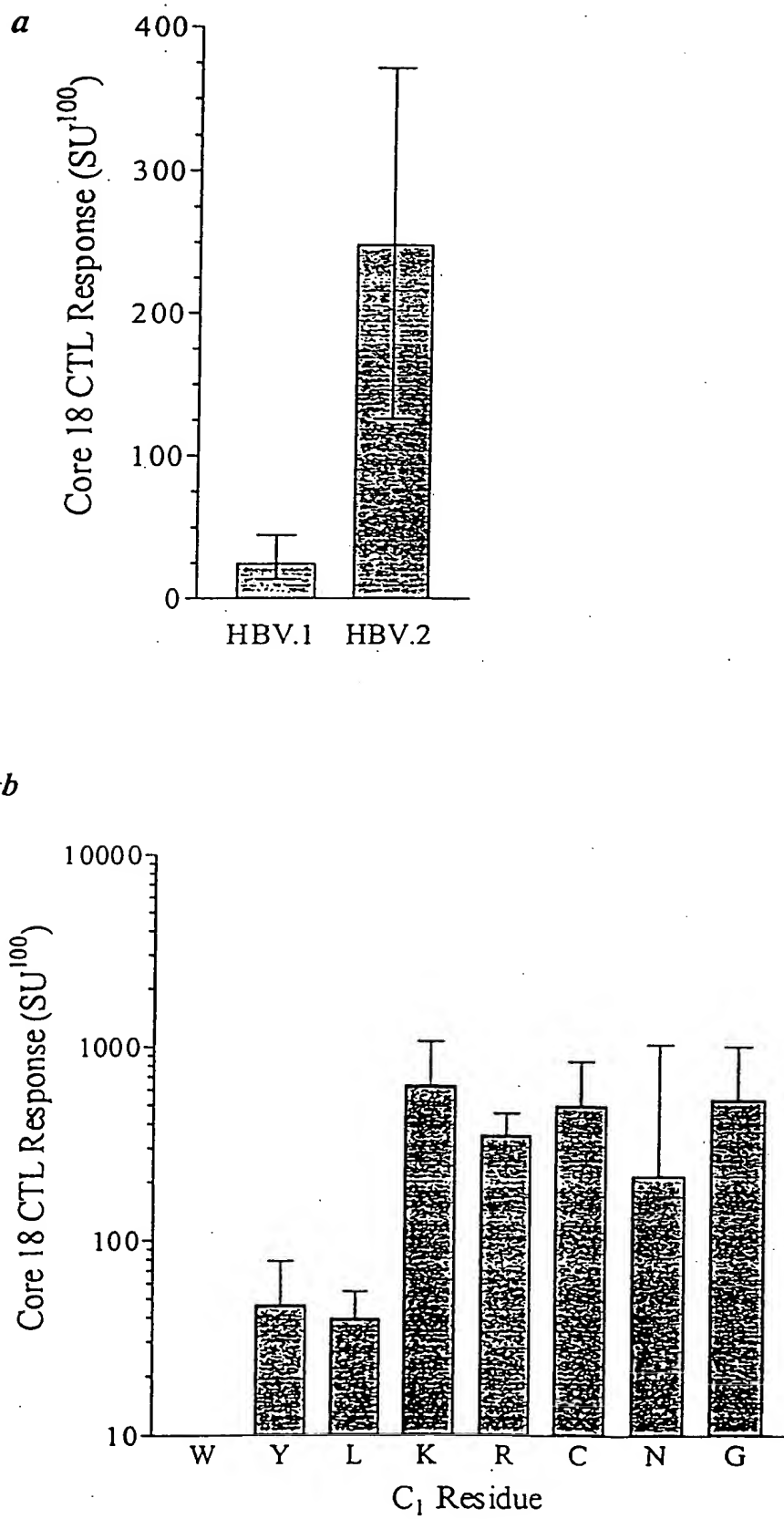


FIGURE 5

FIGURE 6



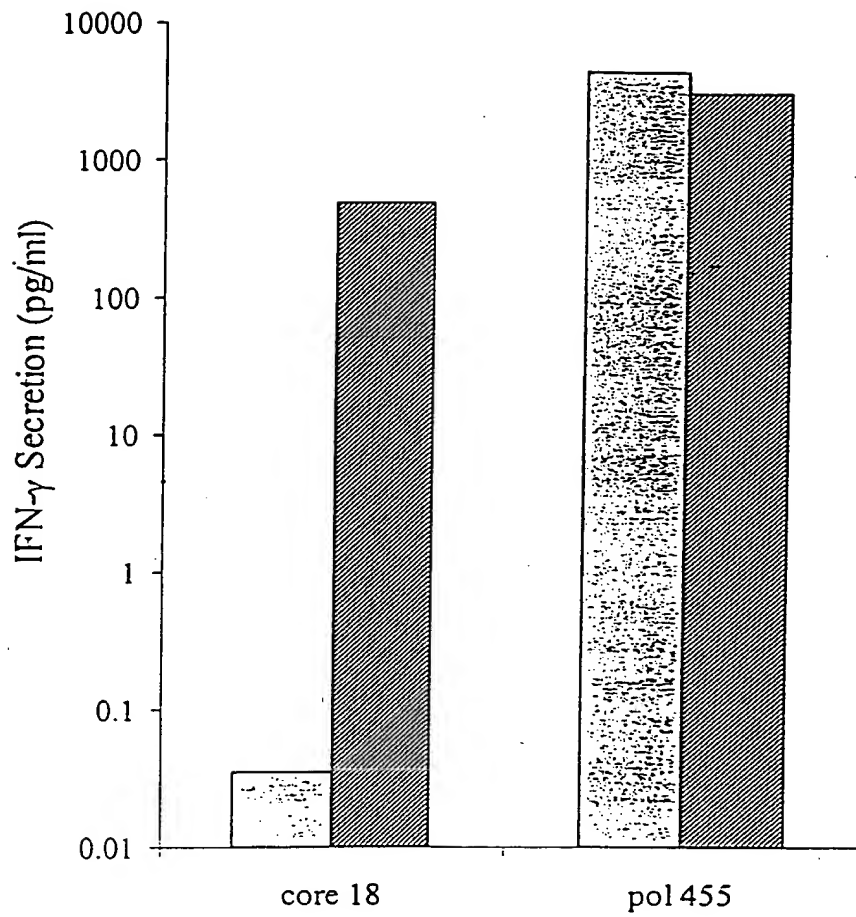


FIGURE 7

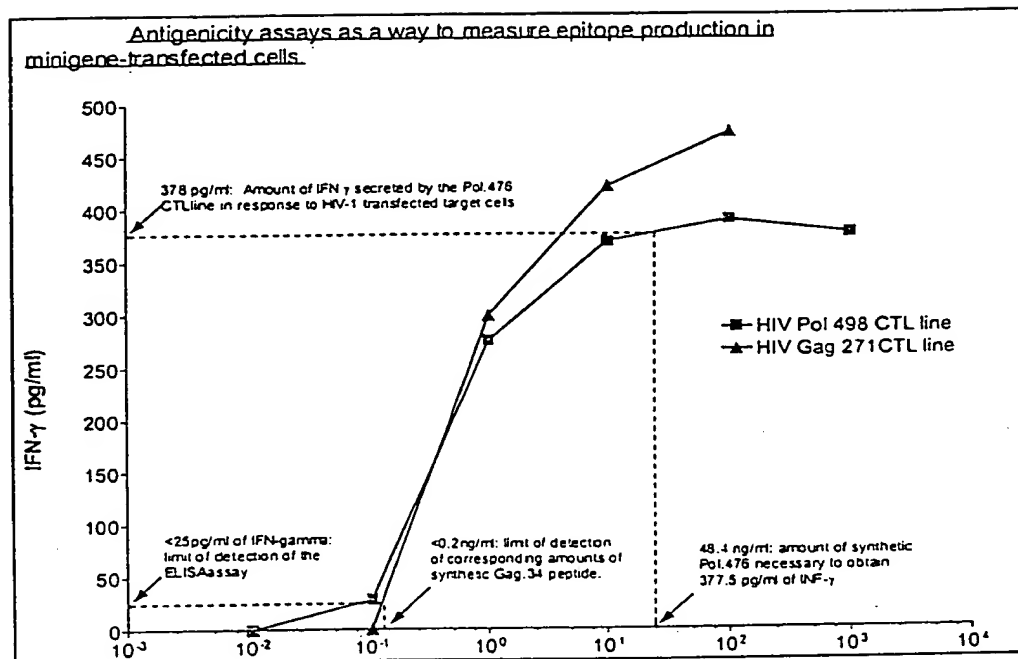


FIGURE 8



EP-HIV-1090

signal	pod 448	AAA	pod 498	env 259	env 259	PADRE	def 94	env 134	gag 386	pod 722	pod 347	env 61
A*0201	A*0201	A*0201	A*0201	A*0201	A*0201	A*0201	A*0201	A*0201	A*0201	A*0201	A*0201	A*0201

Pod 893	gag 237	env 47	env 929	gag 545	def 221	vpr 62	pod 971	pod 98	rev 75	gag 271
B*0701	B*0701	A*1101	B*0701	A*0201	A*0201	A*1101	A*1101	A*1101	B*0701	A*0201

HIV-CPT

signal	env 259	AAA	pod 971	pod 98	PADRE	rev 75	pod 347	env 134	pod 929	pod 722	pod 893	pod 498
B*0701	A*1101	A*1101	A*1101	A*1101	A*0201	A*1101	A*1101	A*0201	A*1101	A*1101	B*0701	A*0201

def 221	gag 386	vpr 62	env 250	env 47	gag 237	gag 545	env 61	pod 448	def 94	gag 271
A*0201	A*0201	A*0201	B*0701	A*1101	B*0701	B*0701	A*1101	A*0201	B*0701	A*0201

HIV-TC

signal	Pod 597	Pod 347	Pod 722	Env 259	Gag 237	Nef 221	Pod 132	Gag 317	Env 61	Gag 162
A*0201	A*0201	A*1101	A*1101	B*0701	B*0701	A*0201	A*0201	A*0201	A*0201	A*1101

Pod 448	Vpr 46	Nef 100	Pod 395	Env 671	Pod 183	Gag 271	Pod 344	Rev 75	Pod 893	Env 651
A*0201	A*0201	A*1101	A*0201	A*0201	A*0201	A*0201	A*0201	B*0701	B*0701	A*0201

Pod 498	Pod 186	Env 55	Pod 92	Pod 533	Gag 386	Pod 103	Pod 664	Env 259	Pod 368	Pod 929
A*0201	B*0701	A*0201	A*1101	A*0201	A*0201	A*0201	A*0201	A*0201	A*0201	A*1101

Pod 530	Vpr 14	Pod 971	Nef 54	Env 681	Vif 7	Pod 879	PADRE	Env 124	Pod 774	Env 163
A*0201	A*0201	A*1101	A*0201	A*0201	A*1101	A*0201	A*0201	A*0201	A*0201	A*0201

Env 47	Vpr 59	Pod 772	Gag 545
A*1101	A*0201	B*0701	

FIGURE 9

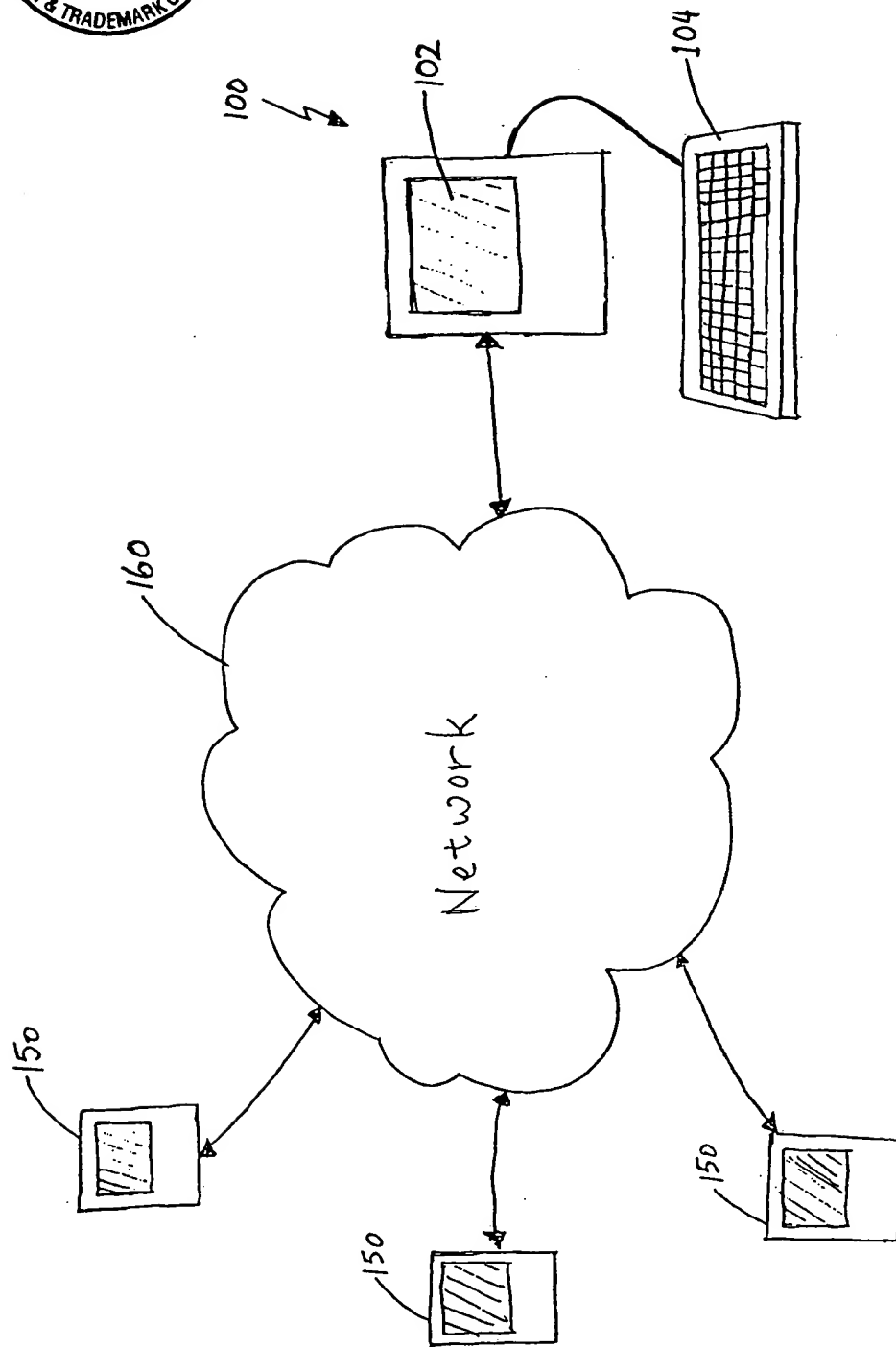


FIGURE 10



200

Sequence	Length	Code
VLA EAMSQV (SEQ ID NO:70)	9	A
ILKEPVHGV (SEQ ID NO:71)	9	B
TLNFPISPI (SEQ ID NO:72)	9	C
SLLNATDIAV (SEQ ID NO:73)	10	D
QMAVFIHNFK (SEQ ID NO:74)	10	E
VTVYYGVPVWK (SEQ ID NO:75)	11	F
FPVRPQVPL (SEQ ID NO:76)	9	G
YPLASLRS LF (SEQ ID NO:77)	10	H
VTYQYMDDL Y (SEQ ID NO:78)	10	I
IYQEPFKNL (SEQ ID NO:79)	9	J
IWGCSGKLI (SEQ ID NO:80)	9	K

202

AA	C+1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

204

Motif Specification

XXXX(FY)XX(LIMV) (SEQ ID NOS:7-14)
 XXXX(FY)XXX(LIMV) (SEQ ID NOS:15-22)
 XXXXNXXX(LIMV) (SEQ ID NOS:27-30)
 XXXXNXXXX(LIMV) (SEQ ID NOS:341-344)
 X(LM)XXXXXXV (SEQ ID NOS:31-32)
 X(LM)XXXXXXV (SEQ ID NOS:33-34)
 X(LMVT)XXXXXX(KRY) (SEQ ID NOS:345-356)
 X(LMVT)XXXXXX(KRY) (SEQ ID NOS:357-368)
 XPXXXXXX(LIMVF) (SEQ ID NOS:59-63)
 XPXXXXXX(LIMVF) (SEQ ID NOS:64-68)

206

FIGURE 11A



MaxInsertions={enter value here} 208
OutputToScreen=yes/no 210
OutputToFile=yes/no 212
MinimumAccepted={enter value here} 214
MaxDuplicateFunctionValues={enter value here} 216
MaxSearchTime (min.)={enter value here} 218
Exhaustive=yes/no 220
NumStochasticProbes={enter value here} 222
MaxHitsPerProbe={enter value here} 224
RandomProbeStart=yes/no 226

FIGURE 11B

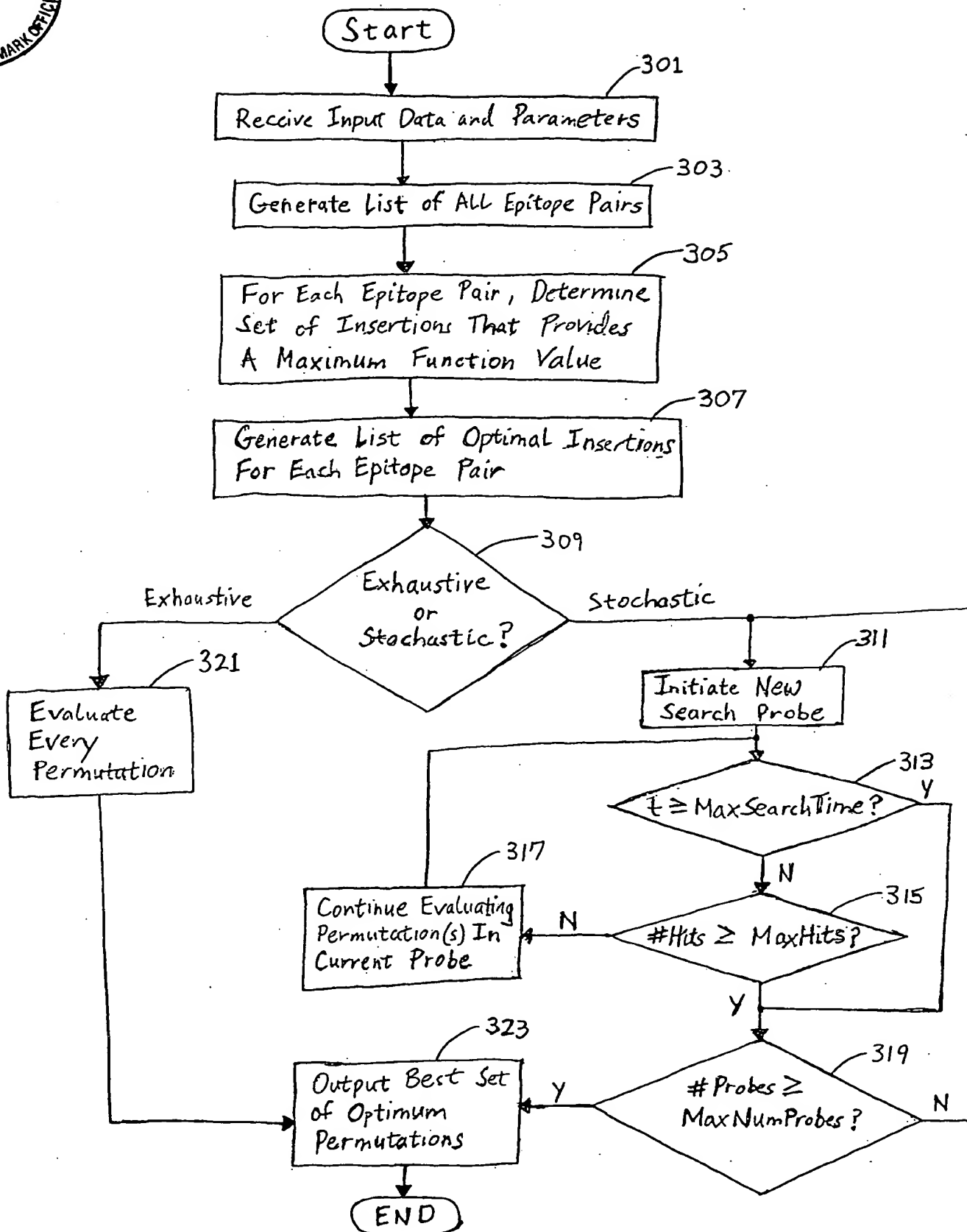


FIGURE 12



Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

204

The following 10 motif specifications will be used to search for junctionals.

Count	Motif Specification
1	XXXX(FY)XX(LIMV) (SEQ ID NOS:7-14)
2	XXXX(FY)XXX(LIMV) (SEQ ID NOS:15-22)
3	XXXNXXX(LIMV) (SEQ ID NOS:27-30)
4	XXXNXXXX(LIMV) (SEQ ID NOS:341-344)
5	X(LM)XXXXXXV (SEQ ID NOS:31-32)
6	X(LM)XXXXXXV (SEQ ID NOS:33-34)
7	X(LMVT)XXXXXX(KRY) (SEQ ID NOS:345-356)
8	X(LMVT)XXXXXX(KRY) (SEQ ID NOS:357-368)
9	XPXXXXXX(LIMVF) (SEQ ID NOS:59-63)
10	XPXXXXXX(LIMVF) (SEQ ID NOS:64-68)

206

Code	Peptide	Length
A	VLAEMSQV (SEQ ID NO:70)	9
B	ILKEPVHGV (SEQ ID NO:71)	9
C	TLNFPISPI (SEQ ID NO:72)	9
D	SLLNATDIAV (SEQ ID NO:73)	10
E	QMAVFIHNFK (SEQ ID NO:74)	10
F	VTVYYGVPVWK (SEQ ID NO:75)	11
G	FPVRPQVPL (SEQ ID NO:76)	9
H	YPLASLRSLF (SEQ ID NO:77)	10
I	VIYQYMDLDY (SEQ ID NO:78)	10
J	IYQEPFKNL (SEQ ID NO:79)	9
K	IWGCSGKLI (SEQ ID NO:80)	9

202

MaxInsertions = 4 (208)

FIGURE 13A



OutputToScreen = No

OutputToFile = Yes

MinimumValueAccepted = 0

MaxDuplicateFunctionValues = 50

SearchTime = 5

NumStochasticProbes = 10

MaxHitsPerProbe = 25

RandomProbeStart = Yes

Col. 1 Code 1	Col. 2 I1	Col. 3 I2	Col. 4 I3	Col. 5 I4	Col. 6 Code 2	Col. 7 C	Col. 8 N	Col. 9 C+N	Col. 10 J	Col. 11 MaxFunc.
A	C	A		L	B	2.00	2.20	4.40	0	8.80
A	C			L	C	2.00	2.20	4.40	0	8.80
A	C			L	D	2.00	2.20	4.40	0	8.80
A	C			L	E	2.00	2.20	4.40	0	8.80
A	C			R	F	2.00	1.57	3.14	2	1.57
A	C			R	G	2.00	1.57	3.14	1	3.14
A	C			R	H	2.00	1.57	3.14	0	6.28
A	G				I	1.80	1.33	2.39	1	2.39
A	C	A	A	G	J	2.00	1.33	2.66	0	5.32
A	C			R	K	2.00	1.57	3.14	0	6.28
B	C	A	A	G	A	2.00	1.33	2.66	0	5.32
B	C	A		R	C	2.00	1.57	3.14	0	6.28
B	C	A		R	D	2.00	1.57	3.14	0	6.28
B	C	A		R	E	2.00	1.57	3.14	0	6.28
B	C		A	G	F	2.00	1.33	2.66	1	2.66
B	C			R	G	2.00	1.57	3.14	1	3.14
B	C			R	H	2.00	1.57	3.14	0	6.28
B	C	A	A	G	I	2.00	1.33	2.66	1	2.66
B	C	A	A	G	J	2.00	1.33	2.66	0	5.32
B	C	A	A	G	K	2.00	1.33	2.66	0	5.32
C	C	A		R	A	2.00	1.57	3.14	1	3.14
C	C			R	B	2.00	1.57	3.14	1	3.14
C	C	A		L	D	2.00	2.20	4.40	1	4.40
C	C			R	E	2.00	1.57	3.14	1	3.14
C	C			R	F	2.00	1.57	3.14	1	3.14
C	C			R	G	2.00	1.57	3.14	1	3.14
C	C	A		R	H	2.00	1.57	3.14	0	6.28
C	C	A		R	I	2.00	1.57	3.14	1	3.14
C	C	A	A	R	J	2.00	1.57	3.14	0	6.28
C	C	A	A	R	K	2.00	1.57	3.14	0	6.28

FIGURE 13B

MAY 24 2004

PATENT & TRADEMARK OFFICE

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
D	C			L	A	2.00	2.20	4.40	0	8.80
D	C			L	B	2.00	2.20	4.40	0	8.80
D	C			L	C	2.00	2.20	4.40	0	8.80
D	C			L	E	2.00	2.20	4.40	0	8.80
D	G				F	1.80	1.33	2.39	0	4.79
D	C			R	G	2.00	1.57	3.14	0	6.28
D	C	A	A	G	H	2.00	1.33	2.66	0	5.32
D	C			L	I	2.00	2.20	4.40	1	4.40
D	C	A		R	J	2.00	1.33	2.66	0	5.32
D	C			L	K	2.00	1.57	3.14	0	6.28
E	C	A	A	L	A	2.00	2.20	4.40	0	8.80
E	C	A	A	L	B	2.00	2.20	4.40	0	8.80
E	C	A	A	L	C	2.00	2.20	4.40	0	8.80
E	C	A	A	L	D	2.00	2.20	4.40	0	8.80
E	C	A		R	F	2.00	1.57	3.14	0	6.28
E	C	A		R	G	2.00	1.57	3.14	0	6.28
E	C	A		R	H	2.00	1.57	3.14	0	6.28
E	C	A	A	L	I	2.00	2.20	4.40	0	8.80
E	C	A		R	J	2.00	1.57	3.14	0	6.28
E	C	A		R	K	2.00	1.57	3.14	0	6.28
F	K	A		L	A	2.20	2.20	4.84	1	4.84
F	K	A	A	G	B	2.20	1.33	2.93	1	2.93
F	K	A	A	G	C	2.20	1.33	2.93	0	5.85
F	K	A	A	G	D	2.20	1.33	2.93	0	5.85
F	K	A		G	E	2.20	1.33	2.93	0	5.85
F	K	A		G	G	2.20	1.33	2.93	1	2.93
F	K	A		G	H	2.20	1.33	2.93	1	2.93
F	K		A	R	I	2.20	1.33	2.93	1	2.93
F	K			R	J	2.20	1.57	3.45	1	3.45
G	C	A		R	K	2.20	1.57	3.45	0	6.91
G	C	A		R	A	2.00	1.57	3.14	1	3.14
G	C			R	B	2.00	1.57	3.14	2	1.57
G	C			R	C	2.00	1.57	3.14	1	3.14
G	C	A		L	D	2.00	2.20	4.40	1	4.40
G	C			L	E	2.00	1.57	3.14	2	1.57
G	C			L	F	2.00	2.20	4.40	4	1.10
G	C			G	H	2.00	1.33	2.66	0	5.32
G	C	A	A	R	I	2.00	1.57	3.14	2	1.57
G	C	A	A	R	J	2.00	1.57	3.14	1	3.14
G	C	A	A	R	K	2.00	1.57	3.14	0	6.28
H	C	A	A	G	A	2.00	1.33	2.66	0	5.32
H	C	A		G	B	2.00	1.33	2.66	1	2.66
H	C	A		G	C	2.00	1.33	2.66	0	5.32
H	C	A		G	D	2.00	1.33	2.66	0	5.32
H	C	A	A	G	E	2.00	1.33	2.66	0	5.32
H	C		A	G	F	2.00	1.33	2.66	1	2.66
H	C		A	R	G	2.00	1.57	3.14	1	3.14
H	C	A	A	G	I	2.00	1.33	2.66	1	2.66
H	C	A		G	J	2.00	1.33	2.66	1	2.66
H	C	A	A	G	K	2.00	1.33	2.66	0	5.32

FIGURE 13C

MAY 24 2004

PAT & TRADEMARK

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
I	K	A	A	G	A	2.20	1.33	2.93	0	5.85
I	K	A	A	G	B	2.20	1.33	2.93	1	2.93
I	K	A		G	C	2.20	1.33	2.93	0	5.85
I	K	A		G	D	2.20	1.33	2.93	0	5.85
I	K	A	A	G	E	2.20	1.33	2.93	0	5.85
I	K	A	A	G	F	2.20	1.33	2.93	1	2.93
I	K	A		R	G	2.20	1.57	3.45	1	3.45
I	K	A	A	G	H	2.20	1.33	2.93	0	5.85
I	K	A	A	G	J	2.20	1.33	2.93	1	2.93
J	K	A	A	R	K	2.20	1.33	2.93	0	5.85
J	K	A	A	R	A	2.20	1.57	3.45	0	6.91
J	K	A	A	R	B	2.20	1.57	3.45	1	3.45
J	K	A		R	C	2.20	1.57	3.45	0	6.91
J	K	A		R	D	2.20	1.57	3.45	0	6.91
J	K	A		R	E	2.20	1.57	3.45	0	6.91
J	K	A	A	R	F	2.20	1.57	3.45	1	3.45
J	K			R	G	2.20	1.57	3.45	2	1.73
J	K			R	H	2.20	1.57	3.45	1	3.45
J	K	A	A	R	I	2.20	1.57	3.45	0	6.91
J	K	A	A	R	J	2.20	1.57	3.45	1	3.45
K	K			R	K	2.20	1.57	3.45	0	6.91
K	K			L	A	2.20	2.20	4.84	0	9.68
K	K			L	B	2.20	2.20	4.84	0	9.68
K	K			L	C	2.20	2.20	4.84	0	9.68
K	K			L	D	2.20	2.20	4.84	0	9.68
K	K	A	A	L	E	2.20	2.20	4.84	0	9.68
K	K	A	A	R	F	2.20	2.20	4.84	0	9.68
K	G				G	2.20	1.57	3.45	1	3.45
K	K				H	1.80	1.33	2.39	0	4.79
K	K			R	I	2.20	1.57	3.45	0	6.91
K	K			L	J	2.20	2.20	4.84	1	4.84
K	K			R		2.20	1.57	3.45	0	6.91

Junctional Analyzer took 142.77 seconds.

FIGURE 13D



Figure 3a: CTL responses induced by EP HIV-1090 relative to individual peptides in IFA

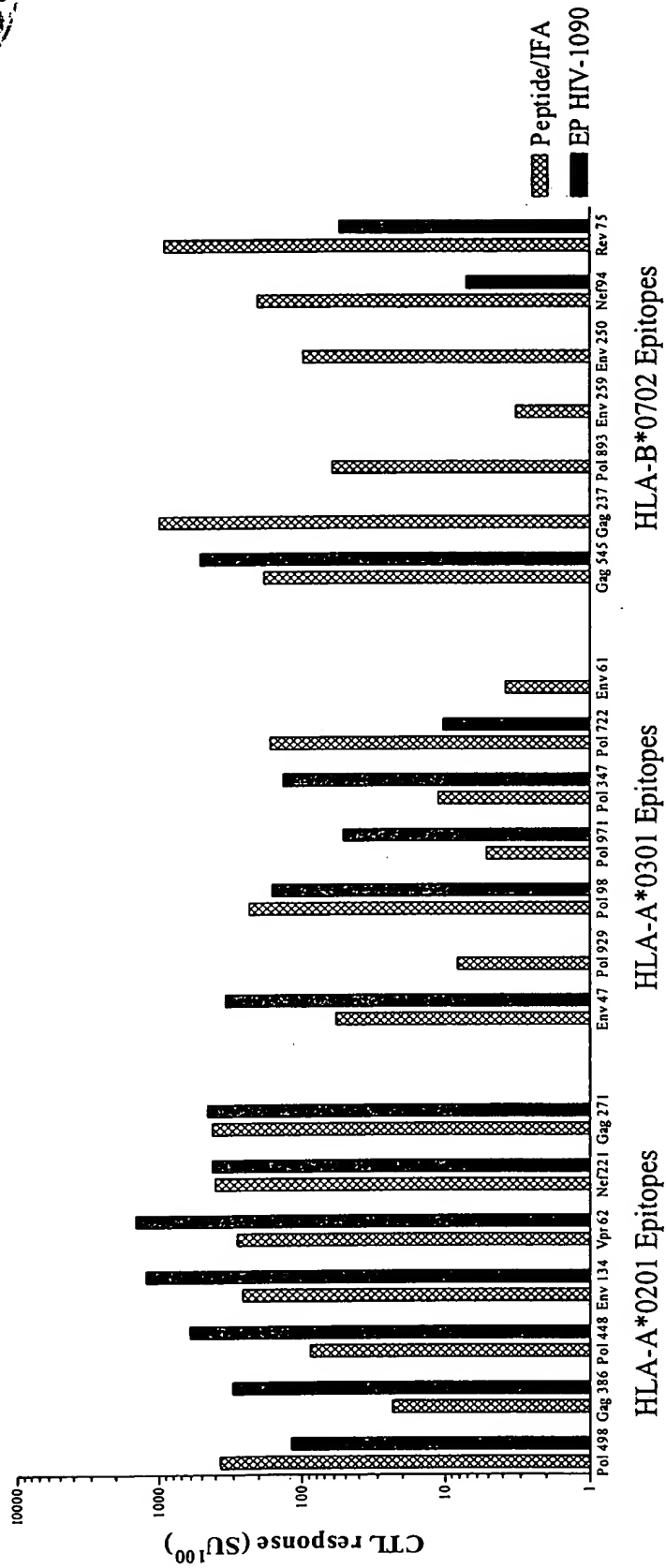


FIGURE 14A

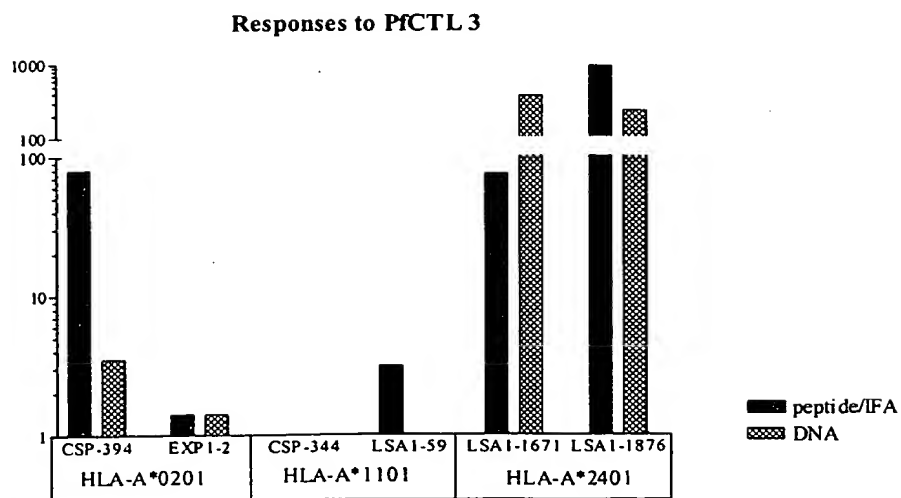
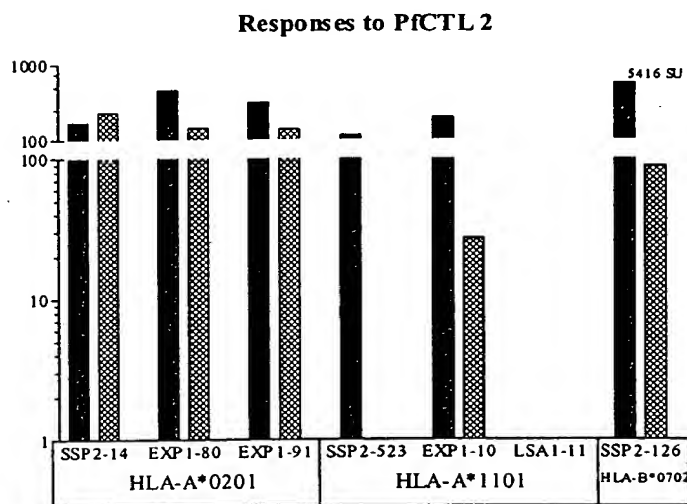
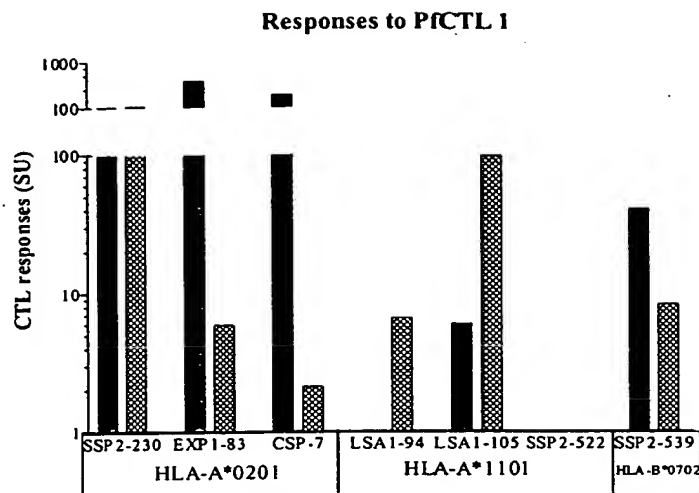


FIGURE 14B

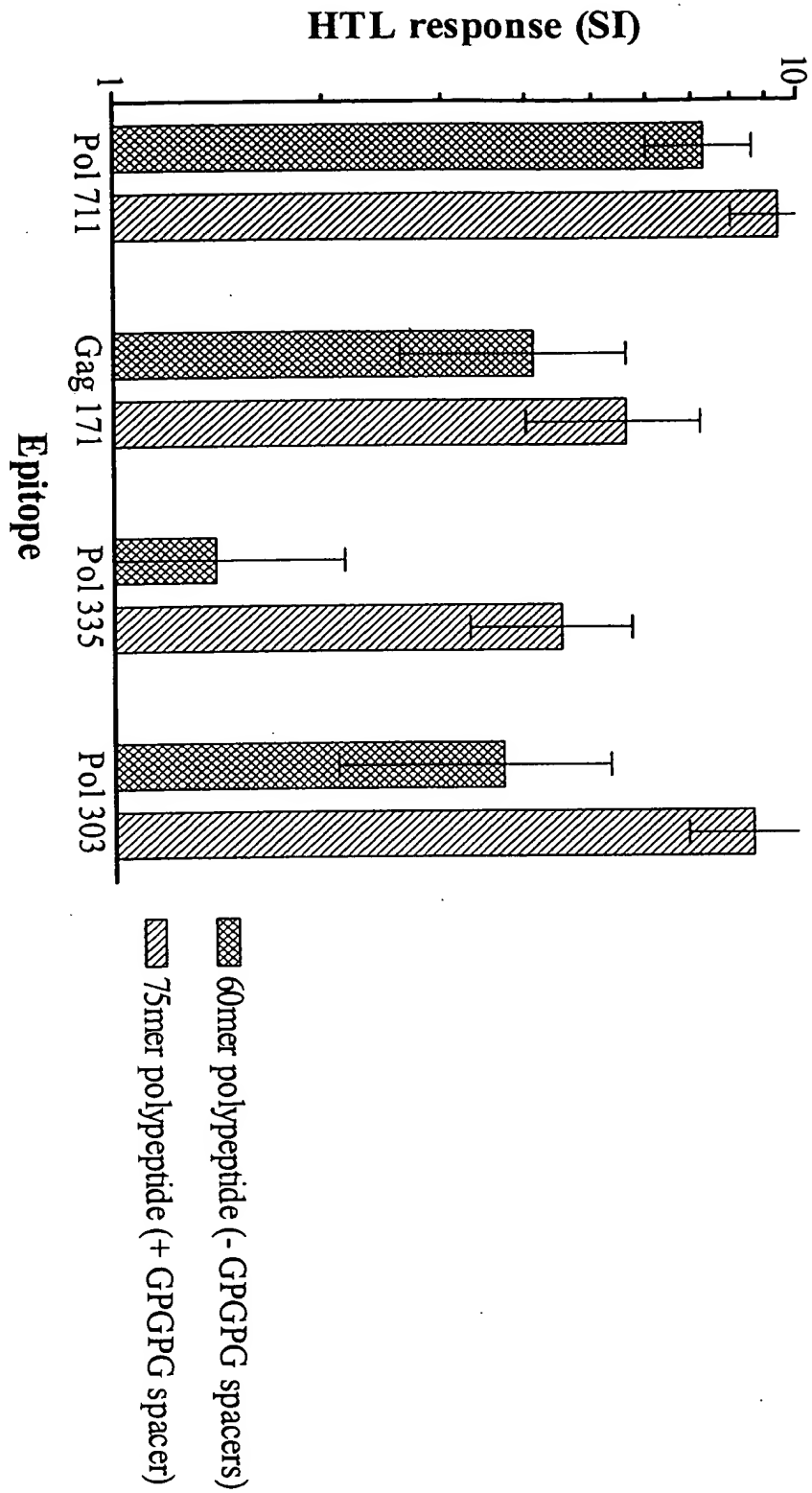


FIGURE 15

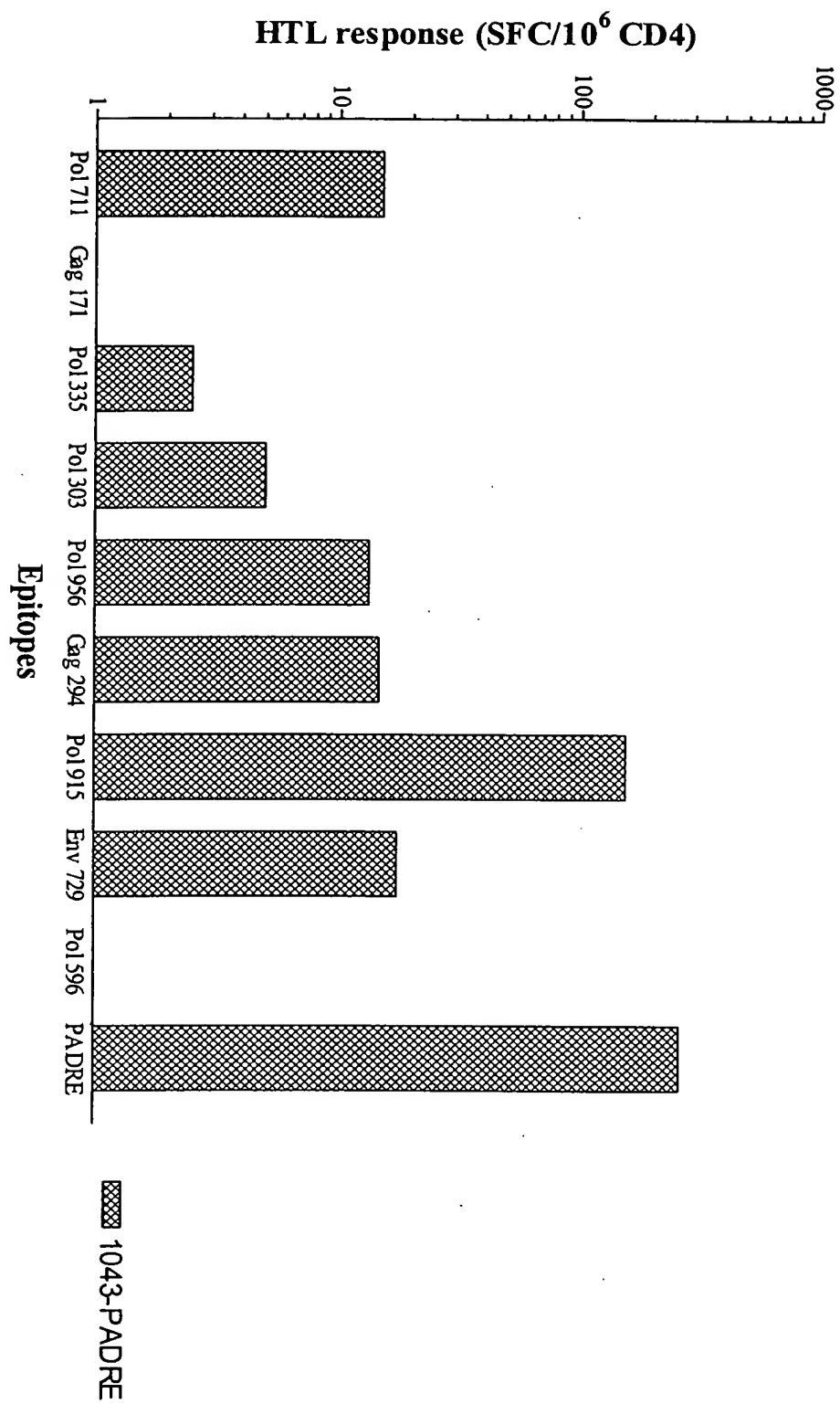


FIGURE 16



HIV 75mer

Pol 711	GAG	Pol 171	GAG	Pol 335	GAG	Pol 303
---------	-----	---------	-----	---------	-----	---------

EP HIV-1043

Pol 711/712	GAG	Pol 956	GAG	Pol 596	GAG	Vpu 31	GAG	Env 729	GAG	Gag 294/298	GAG	Gag 171	GAG	Env 566	GAG	Pol 874	GAG	Pol 915	GAG	Pol 335	GAG	Pol 674	GAG	Pol 758	GAG	Pol 619	GAG	Pol 989	GAG	Pol 303
-------------	-----	---------	-----	---------	-----	--------	-----	---------	-----	-------------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------

EP HIV-1043

Pol 711/712	GAG	Pol 956	GAG	Pol 596	GAG	Vpu 31	GAG	Env 729	GAG	Gag 294/298	GAG	Gag 171	GAG	Env 566	GAG	Pol 874	GAG	Pol 915	GAG	Pol 335	GAG	Pol 674	GAG	Pol 758	GAG	Pol 619	GAG	Pol 989	GAG	Pol 303	GAG	PADRE
-------------	-----	---------	-----	---------	-----	--------	-----	---------	-----	-------------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	---------	-----	-------

FIGURE 17



EP-HIV-1090 (SEQ ID NO:81)

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPIKPIHYCAPA
KAKFVAAWTLKAAAKAFPVRPQVPLGAAKLTPLCVTLGAAAVLAEAMSQVKVYLAWVPAHKG
AAAAIFQSSMTKKTTLFCASDAKNIPYNPQSQGVVKHPVHAGPIANVTVYYGVPVWKAAAQMA
VFIHNFKNAAA YPLASLRSFLNLTFGWCFKLNRLQQLLFINAKIQNFRVYYRKA AVTIKIGGQLKK
VPLQLPPLKAMTNNPPIPV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAAGCTGGTGGGCAAACTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGG
GGTGAATGCCGCTTGCCCTAAAGTCAGCTTCGAACCAATTAAGATCCCCATTCACTACTGTGC
ACCTGCCAAAGCTAAGTTTGTGGCCGCTTGACCCTCAAGGCCGCTGCAAAAGCCTTCCAGT
GAGGCCCCAGGTGCCTCTGGGCGCCGCTAAACTCACACCACTGTGCGTCACTCTGGGAGCCGC
TGCAGTGCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCGCCACAA
GGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAACAACCTCTGTTCTGTGCTC
CGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGC
CGGACCTATTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACA
GATGGCCGTGTTTATTACAAATTTCAAAAACGCCGCTGCATACCCCTCGCCAGCCTGAGATC
CCTCTTCAACCTGACATTCGGCTGGTGTCTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTTT
ATCAATGCTAAATCCAGAACTTCCGCGTCTACTATAGGAAGGCTGCAGTGACTATCAAAATT
GGCGGACAACTGAAGAAAGTGCTCTCCAGCTGCCCCCTCTCAAGGCAATGACCAACAATCC
CCCTATCCCAGTCTGA (SEQ ID NO:82)

HIV-CPT (SEQ ID NO:83)

MGMQVQIQSLFLLLLWVPGSRGIPHYCAPAKAAKIQNFRVYYRKA AVTIKIGGQLKKAKFVAAW
TLKAAAKVPLQLPPLKAIFQSSMTKLTPLCVTLGAQMAVFIHNFKGAKVYLAWVPAHKNAIPYN
PQSQGVVKAILKEPVHGVGAAALTFGWCFKLNVLAEAMSQVNRILQQLLFINAAACPKVSFEPI
KVTVYYGVPVWKKAAHPVHAGPIANAAA YPLASLRSFLNAAATTLFCASDAKNKLVGKLNWAN
AAAFPVRPQVPLNMTNNPPIPV

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAATCCCCATTCACTACTGCGCCCCCTGCTAAGGCAGCCAAAATCCAGAACTTCAGGGTGTAT
TACAGAAAGGCTGCAGTCACCATTAATAATCGGCGGACAACTGAAGAAAGCCAAGTTTGTGGC
CGCTTGACACTCAAGGCCGCTGCAAAGGTCCCACTGCAGTCCCCCTCTGAAGGCCATCTT
CCAGAGCTCCATGACTAAGAAACTGACCCCACTGTGTGTGACACTCGGGGCCAGATGGCTGT
GTTCATCCATAATTTTAAAGGCGCCAAGGTCTACCTGGCTTGGGTGCCCGCACACAAGAAGCG
CATTCCTTACAATCCACAGTCTCAAGGAGTGGTCAAAGCTATTCTGAAGGAGCCCGTGCACGG
GGTGGGCGCCGCTGCACTCACTTTCCGATGGTGTCTTAAACTGAACGCCGCTGCTGGCTGAAGC
CATGAGCCAGGTCAATCGGATCCTGCAGCAACTGCTCTTCAATTAACGCCGCTGCATGTCCTAA
GGTGTCTTCGAGCCAATCAAAGTGACCGTGTATTACGGGGTCCCCGTGTGGAAGAAAGCCGC
TCATCCTGTCCACGCAGGCCCAATCGCCAACGCCGCTGCATATCCCCTCGCCTCTCTGCGCAG
CCTGTTTAAACGCCGCTGCAACAACCTCTTTTGGCCTCCGACGCTAAGAATAAACTGGTGGG
AAAGCTGAAGTGGGCCAACGCAGCTGCATTCCTGTGAGGCCACAGGTCCCCCTCAATATGAC
TAACAATCCCCCTATCCCAGTGTGA (SEQ ID NO:84)

FIGURE 18A



HIV-FT (SEQ ID NO:85)

MQVQIQSLFLLLLWVPGSRGKLVGKLNWAMASDFNLPPVAIFQSSMTKVTIKIGGQLKRILQQLLF
IMAVFIHNFKIPYNPQSQGVVTTLFCASDAKILKEPVHGVQMAVFIHNFKGA VFIHNFKRCPKVSF
EPIKIQNFRVYYRLTFGWCFKLQVPLRPMTYKMTNPPIPVTVYYGVPVWKVLAEAMSQVPIHY
CAPAKLTPLCVTL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGAGGAAAG
CTGGTGGGGAAGCTGAACTGGGCCATGGCCAGCGATTTCAACCTGCCCCCGTGGCCATCTTC
CAGAGCAGCATGACCAAGGTGACCATCAAGATCGGGGGGCAGCTGAAGAGGATCCTGCAGCA
GCTGCTGTTTCATCATGGCCGTGTTTCATCCACAACCTTCAAGATCCCCTACAACCCCCAGAGCCA
GGGGGTGGTGACCACCCTGTTCTGCGCCAGCGATGCCAAGATCCTGAAGGAGCCCGTGACG
GGGTGCAGATGGCCGTGTTTCATCCACAACCTTCAAGGGCGCCGCGTGTTCATCCACAACCTTCA
AGAGGTGCCCCAAGGTGAGCTTCGAGCCCATCAAGATCCAGAACTTCAGGGTGTACTACAGG
CTGACCTTCGGGTGGTGCTTCAAGCTGCAGGTGCCCCCTGAGGCCCATGACCTACAAGATGACC
AACAACCCCCCATCCCCGTGACCGTGTACTACGGGGTGCCCGTGTGGAAGGTGCTGGCCGAG
GCCATGAGCCAGGTGATCCCCATCCACTACTGCGCCCCCGCCAAGCTGACCCCCCTGTGCGTG
ACCCTG (SEQ ID NO:86)

FIGURE 18B



HIV-TC (SEQ ID NO:87)

MGMQVQIQSLFLLLLWVPGSRGYWQATWIPWKAIFQSSMTKKVYLAWVPAHKNAACPKVSFE
PIKHPVHAGPIANLTFGWCFKLNKMIGGIGGGFIKFRDYVDRFYKAAARILQQLLFINTTLFCASDAK
NQMVHQAI SPRGAKLVGKLNWAGAAAIYETYGDTWKAAQVPLRPMTYKGAAAVTVLDVGDAY
NAAARYLKDQQLNLNFPISPINMTNPPIPVNAPYNTPVFAIKAAAVPLQLPLKAAIPYNPQSQ
GVVKALLQLTVWGIGAILKEPVHGVNAAAFPISPIETVKVWKEATTTLFKAAAVTIKIGGQLKKI
YQEPFKNLKAAAVLAEAMSQVNLVGPTPVNIGAAAEVNIVTDSQYKAAAPIHYCAPAKAVIYQY
MDDLKAAAQMAVFIHNFKNAAATYQIYQEPFKPYNEWTLKAKIQNFRVYYRKAFVVRPQVPL
GAAAIWGC SGKLIKVMIVWQVDRNAAKAACWWAGIKAKFVAAWTLKAAAKLTPLCVTLNAAM
ASDFNLPPVKSLLNATDIAVNVTVYYGVPVWKKAAAAIIRILQLKRAMASDFNLNAAAYPLASL
RSLF

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGATCTAGA
GGATACTGGCAAGCTACTTGGATTCCAGAATGGAAAGCTATCTTTCAATCCTCAATGACGAAG
AAGGTATACCTGGCATGGGTCCCAGCACACAAGAACGCCGCTTGCCCAAAGGTGTCCTTTGAA
CCCATTAACACCCAGTGCACGCAGGGCCAATAGCGAATTTGACATTCGGGTGGTGCTTCAAA
CTAAACAAAAATGATCGGCGGCATTGGAGGCTTTATCAAGTTTAGAGATTACGTGGACCGATT
TATAAAGCCGCTGCCGTATACTCCAGCAGCTACTATTCAACACCACTCTCTTCTGCGCTT
CAGACGCTAAGAACCAAATGGTACACCAAGCCCTAGAGGAGCCAAGCTCGTAGGG
AAATTAATTTGGGCGGGTGCAGCAGCAATCTACGAGACTTACGGCGATACCTGGAAAGCAGC
CCAGGTTCCGTTACGCCAATGACCTATAAAGGCGCAGCAGCAGTAACAGTTCTAGATGTAGG
AGACGCTTACAACGCTGCCGCAAGATACCTAAAAGATCAGCAGTTACTCAACACACTAAATTT
CCCAATTAGCCCGATAAACATGACAAATAACCCACCAATTCCCGTCAATGCTCCCTACAACAC
TCCAGTATTCGCAATCAAAGCCGCTGCTGTCCCCCTGCAGCTCCCTCCTCTGAAAGCTGCGAT
ACCTTACAACCCACAGAGCCAAGGTGTTGTCAAAGCACTGCTTCAGCTAACAGTTTGGGGAAT
TGGTGCTGCAATTCTAAAAGAGCCAGTTCATGGGGTTAACGCCGCCGCTTCCCAATCAGTCC
TATTGAGACTGTGAAAGTATGGAAAGAAGCCACAACCACACTTTTTAAGGCAGCCGCAGTTA
CAATTAATAATAGGGGGCCAACTTAAGAAAAATATACCAGGAACCTTTCAAGAATCTCAAAGCC
GCTGCAGTGCTCGCCGAGGCTATGTACAGGTGAATTTGGTCGGACCAACACCCGTAAACATC
GGAGCCGCAGCCGAAGTGAACATAGTCACCGACTCACAGTACAAAGCCGCTGCAATACCCAT
ACATTATTGTGCTCCCGCAAAGGCCGTGATCTATCAATATATGGACGACCTGTATAAGGCCGC
CGCGCAGATGGCAGTCTTTATCCACAACCTTTAAAAACGCAGCTACTTATCAGATCTACCAGGA
ACCATTCAAACCGTACAATGAGTGGACCTTGGAATAAAGGCCAAAATTCAGAACTTCAGGG
TATATTATAGAAAAGCATTTCCAGTGAGGCCCCAGGTGCCTCTGGGTGCCGCAGCAATATGGG
GATGTTCTGGAAAAGTATCAAGGTGATGATTGTATGGCAAGTGGACAGAAATGCAGCTAAG
GCAGCCTGTTGGTGGGCAGGTATAAAGCAAAGTTCGTGGCAGCATGGACGCTTAAAGCAGC
CGCAAAACTCACTCCTCTCTGCGTGACACTTAATGCAGCCATGGCCTCTGATTTCACCTTCCC
CCTGTAAAATCCCTGCTTAATGCGACAGATATCGCAGTCAACGTAACAGTATATTATGGCGTG
CCAGTCTGGAAAAAAGCCGCCGCGGCCATAATTCGGATACTGCAGCAGCTGAAAAGAGCTAT
GGCGAGTGACTTCAACCTGAATGCGGCCGCTACCCCTTGGCATCGTTAAGGTCATATTTTG
A (SEQ ID NO:88)

FIGURE 18C



HCV.1 (SEQ ID NO:89)

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVDLMGYIPLVYLVAAYQATVILAGYGAGVRLIVFP
DLGVHMWNFISGIYLLPRRGPRLYLVRHADVVLVGGVLAALLFLLLADAFLLLADARVWMNRL
IAFACTCGSSDLYLSAFSLHSYGVAGALVAFKLPGCSFSIFKTSERSQPRLIFCHSKKKFWAKHMW
NFIPFYGKAIRMYVGGVEHRQLFTFSRRRLGVRATRKVGIYLLPNRAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGACTGC
TGTTCAACATCCTGGGGGGTGGGTGGATCTGATGGGTACATCCCCCTGGTGTACCTGGTGGCCTACCAGGCCACCGT
GATCCTGGCCGGGTACGGGGCCGGGTGAGGCTGATCGTGTTCCTGCTGCTGGGTGCACATGTGGAACCTTCATCAGC
GGGATCTACCTGCTGCCAGGAGAGGACCTAGACTGTACCTGGTACTAGACACGCTGATGTGGTGTCTGGTGGGAGGAG
TGCTGGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTTTCCTGCTGCTGGCTGATGCTAGAGTGTGGATGAACAGACT
GATCGCTTTTCGCTTGTACATGTGGAAGCTCCGATCTGTATCTGAGCGCTTTCAGCCTGCACAGCTACGGAGTGGCTGGA
GCTCTGGTGGCTTTTAAGCTGCCTGGATGTAGCTTTAGCATCTTTAAGACCAGCGAAAGAAGCCAGCCTAGACTGATCT
TTTGTACAGCAAGAAGAAGTTTGGGCTAAGCACATGTGGAATTTTATCCCTTTCTATGGAAAGGCTATCAGAATGTA
TGTGGGAGGAGTGGAAACACAGACAGCTGTTTACATTTAGCCCTAGAAGGAGACTGGGAGTGAGAGCTACAAGAAAGGTG
GGAATCTATCTGCTGCCTAATAGATGAAAGCTTGGG* (SEQ ID NO:90)

HCV.2 (SEQ ID NO:91)

MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAALLFLLLADALIFCHSKKKQLF
TFSPRRYLVRHADVYLLPRRGPRLCTCGSSDLYHMWNFISGIFWAKHMWNFAKFVAAWTLKAA
AILAGYGAGVYLVAAYQATVGVAGALVAFKIPFYGKAIRMYVGGVEHRVLVGGVLAALFLLLADA
RVLPGCSFSIFAKFVAAWTLKAAAKTSERSQPRRLGVRATRKRLIVFPDLGVWMNRLIAFALSAFS
LHSYLLFNILGGWVVGIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGATCTGATGGGATATATCCCTCTGGTGGCTAAGTTTGTGGCTGCT
TGGACACTGAAAGGCTGCTGCTGCTGTTTCTGCTGCTGGCTGATGCTCTGATCTTCTGTGTCACA
GCAAGAAGAAGCAGCTGTTTACATTTAGCCCAAGAAGATATCTGGTGACAAGACACGCTGAT
GTGTATCTGCTGCCTAGACGCGGACCTAGACTGTGTACATGTGGAAGCTCCGATCTGTATCAC
ATGTGGAACCTTTATCAGCGGAATCTTTTGGGCTAAGCACATGTGGAATTTTCATCCTGGCTGGA
TATGGAGCTGGAGTGTATCTGGTGGCTTATCAGGCTACAGTGGGAGTGGCTGGAGCTCTGGTG
GCTTTCAAGATCCCATTCTATGGAAAGGCTATCAGAATGTATGTGGGAGGAGTGGAAACACAG
AGTGCTGGTGGGAGGAGTGTGGCTGCTTTCTGCTGCTGGCTGATGCTAGAGTGTGCTGCCAGG
ATGTAGCTTTAGCATCTTCAAGACTTCCGAACGCTCCAGCCTAGAAGACTGGGAGTGAGAGC
TACAAGGAAGAGACTGATCGTGTTCAGATCTGGGAGTGTGGATGAATAGACTGATCGCTTT
CGCTCTGAGCGCTTTCAGCCTGCACAGCTATCTGCTGTTCAACATCCTGGGAGGATGGGTGGT
GGGAATCTATCTGCTGCCAAACAGATGAAAGCTT (SEQ ID NO:92)

HCV.3s1 (SEQ ID NO:93)

MGMQVQIQSLFLLLLWVPGSRGYLVAYQATVAKFVAAWTLKAAALLFLLLADALIFCHSKKKYL
VTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNF*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGATACCTCGTCGCCTACCAGGCCACTGTGGCTAAATTCGTGGCAGCC
TGGACACTGAAAGCTGCAGCTCTGCTCTTCTGCTCCTGGCCGATGCACTCATCTTCTGCCATT
CCAAGAAAAAGTATCTGGTCAACAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGC
AAGTGACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACCTTTATTTCTGGAATCTTTTGGG
CCAAGCACATGTGGAATTTCTGAAAGCTT (SEQ ID NO:94)

FIGURE 18D



HCV.3s2 (SEQ ID NO:95)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYIL
AGYGAGVWMNRLIAFAIPFYGKAIVAGALVAFKVGIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCCGATCCAGAGGAGTCCTGGTGGCGGCGTCCTGGCCGCTGCTAAGTTTGTGCGCTGCT
TGGACACTGAAGGCAGCCGCTTCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT
GCCATTCCATTCTATGGGAAAGCCATTGTGGCTGGCGCCCTGGTGGCATTCAAGGTCGGGATC
TACCTCCTGCCTAACCCTGAAAGCTT (SEQ ID NO:96)

HCV.3s2(-3) (SEQ ID NO:97)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYIL
AGYGAGVWMNRLIAFA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCCGATCCAGAGGAGTCCTGGTGGCGGCGTCCTGGCCGCTGCTAAGTTTGTGCGCTGCT
TGGACACTGAAGGCAGCCGCTTCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT
GCCTGAGGATCC (SEQ ID NO:98)

HCV.3s3 (SEQ ID NO:99)

MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAARLGVRATRKLLFNILGGWV
RMVYGGVEHRRLLIVFPDLGVGVAGALVAFKLPGSFSIFKTSERSQPRQLFTFSPPRYLLPRRGPRL

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCCGATCCAGAGGAGACCTGATGGGCTACATCCCTCTCGTGGCCAAGTTTGTGGCAGCT
TGGACCCTGAAGGCCGCTGCCAGACTGGGAGTGCGCGCTACACGGAAACTCCTGTTTAACATC
CTGGGAGGGTGGGTGCGGATGTACGTCGGAGGCGTCGAGCACAGAAGGCTCATTGTCTTTCC
AGATCTCGGCGTGGGCGTCGCAGGCGCACTCGTGGCCTTCAAACCTGCCAGGGTGACGCTTCAG
CATTTTCAAGACCTCCGAACGCTCCCAACCCAGACAGCTGTTCACTTTCTCTCCTCGGAGGTAT
CTGCTGCCAGACGCGGACCCAGGCTGTGAAAGCTT (SEQ ID NO:100)

HCV.PC3 (SEQ ID NO:101)

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVKAKFVAAWTLKAAALADGGCSGGAYRLIVFPD
LGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPPR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCCGATCCAGAGGACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCCAAGTTCGTG
GCTGCCTGGACCCTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCGGAGCTTACAG
GCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGAATTTTCATCGG
GGTGGCCGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTACCTTCTCCCAAGACGGTGAGG
TACC (SEQ ID NO:102)

FIGURE 18E



HCV_PC4 (SEQ ID NO:103)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAKFVAAWTLKAAAKTSERSQPRNLPGCSFSIFN
DLMGYIPLVKYLLPRRGPRLNTLCGFADLMGYRMYVGGVEHR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCCGGATCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCCAAGTTCGTGGC
TGCTGGACCTGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTG
GATGCTCTTTACGATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCC
CAGACGGGGCCCTCGCCTGAAOACTCTCTGTGGATTGCTGATCTGATGGGGTACAGGATGTA
TGTCGGCGGAGTCGAACACAGATGAGGTACC (SEQ ID NO:104)

HCV_2431(1P) (SEQ ID NO:105)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAFAFLLADARVLSAFSLHSYILAGYGAGVWMNRL
IAFAGAAARLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPRRGPRLNTLCG
FADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGA YRLIVFPDLGVKFWAKHMWN
FIGVAGALVAFKKQLFTFSPPRNGYLVA YQATVAAALLFLLADALIFCHSKKKYL VTRHADVLG
FGAYMSKCTCGSSDL YHMWNFISGIFWAKHMWNFKAAA AKFVAAWTLKAAA

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCCGGCTCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCA
GACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGC
GTGTGGATGAATCGGCTGATCGCCTTTGCCGGCGCTGCCGCAAGGCTGGGCGTGAGAGCCACC
CGGAAGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTC
TTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGG
GGCCCTCGCCTGAACACTCTCTGTGGATTGCTGATCTGATGGGGTACAGGATGTATGTCCGC
GGAGTCGAACACAGAAAACCTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCT
GGCCGACGGGGGATGCAGCGGCGGAGCTTACAGGCTCATTGTCTTCCCGATCTCGGAGTCAA
ATTTTGGGCAAAGCACATGTGGAATTTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAA
GCAGCTCTTCACCTTCTCCCCAAGACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGC
TGCAGCTCTGCTCTTCTGCTCCTGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTAT
CTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGC
AGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGG
AATTTTAAGGCCGACGAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGG
ATCC (SEQ ID NO:106)

FIGURE 18F



HCV.4312(1P) (SEQ ID NO:107)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK
YLLPRRGPRNLNLCGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFP
DLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHS
KKKYLVTNRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLAA
AFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFANAAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCCGGCTCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAC
AAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCAT
GGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGCCTGAACACTCTCTG
TGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGAAAACTGCT
CTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCG
GAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGA
ATTTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAA
GACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTTCTGCTCC
TGGCCGATGCACCTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACG
TGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGT
GGAACCTTTATTTCTGGAATCTTTTGGGCAAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAG
TCCTGGTGGGCGGCGTCTGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGTGTCTG
CCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGA
TCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAG
GATCC (SEQ ID NO:108)

AOSL.K (SEQ ID NO:109)

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPDFFPSVKFLLSLGIH
LYMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWLSLLVPFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAAGTTCCTGCTGTCCCTGGGAA
TCCACCTGTATATGGATGACGTGGTGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT
TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGGCCTTTGTGTGA (SEQ ID NO:110)

HBV.1 (SEQ ID NO:111)

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPDFFPSVFLSLGIHL
YMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWLSLLVPFVIPSSWAFTP
ARVTGGVFKVGNFTGLYLPSDFFPSVTLWKAGILYKNVSIPWTHKLVDVFSQFSRSAICSVVRRAL
MPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGTTCCTGCTGTCCCTGGGAATCC
ACCTGTATATGGATGACGTGGTGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCC
TGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCCT
TCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGGCCTTTGTGATCCCTATCCCTAG
CTCCTGGGCTTTACCCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAAACTTCACCGG
CCTGTATCTGCCAGCGATTTCTTTCCTAGCGTGACCCTGTGGAAGGCCGGGATCCTGTACAA
GAATGTGTCCATCCCTTGGACCCACAAGCTGGTGGTGGACTTTTCCAGTTCAGCAGATCCGC
TATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGTATGCCTGTATCTGA (SEQ ID NO:112)

FIGURE 18G



HBV.2 (SEQ ID NO:113)

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFPSDFFPVSFNLLSLGIH
LYMDDVVLGVLSRYVARLFLLTRILTISTLPETTIVRRQAFTFSPTYKGAAAWLSLLVPFVNPIIP
SSWAFKTPARVTGGVFKVGNFTGLYNLPDFFPSVKTLWKAGILYKNVSIPWTHKGAALVDFSQ
FSRNSAICSVVRRALMPYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAACCTCCTGCTGTCCCTGGGAA
TCCACCTGTATATGGATGACGTGGTGTCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT
TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGT
GAATATCCCTATCCCTAGCTCCTGGGCTTTCAGACCCCAAGCCAGGGTGACCGGAGGAGTGTT
TAAGGTGGGAAACTTCACCGGCCTGTATAACCTGCCAGCGATTTCTTTCCTAGCGTGAAGAC
CCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCG
CTCTGGTGGTGGACTTTTCCAGTTCAGCAGAAATCCGCTATCTGCTCCGTGGTGAGGAGAG
CTCTGATGCCACTGTATGCCTGTATCTGA (SEQ ID NO:114)

PfCTL.1 (SEQ ID NO:115)

MQVQIQSLFLLLLWVPGSRGILSVSSFLFVNAAAQTNFKSLLRNLPSENERGYKAAALLACAGLAY
KAAAAKFVAAWTLKAAAKAFMKAVCDEVNAAASFLFVEALFNATPYAGEPAPFKAAAKYKLA
TSVLKAGVSENIFLNAAAAYFILVNLLIKAGLLGVSTV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAATCCTGAGCGTGTCTCTTTCTGTTTGTCAACGCCGCTGCACAGACCAATTTCAAGAGC
CTCCTGAGGAACCTCCCTCCGAGAACGAAAGAGGCTACAAAGCCGCTGCACTGCTCGCCTGC
GCTGGACTGGCCTATAAGAAAGCCGCTGCAGCCAAGTTCGTGGCCGCTTGGACACTGAAGGC
CGCTGCAAAAGCCTTTATGAAGGCTGTCTGTGTGGAGGTCAATGCCGCTGCATCTTTCCTGTTT
GTGGAGGCCCTCTTTAACGCTACTCCTTACGCAGGGGAACCAAGCCCTTCAAGGCCGCTGCA
AAATATAAGCTGGCAACCAGCGTGTCTGAAGGCTGGCGTGTCCGAGAATATTTTTCTGAAAAAC
GCCGCTGCATACTTCATCCTGGTGAATCTGCTCATTAAAGGCCGACTCCTGGGGGTGGTCTCT
ACAGTGTGA (SEQ ID NO:116)

PfCTL.2 (SEQ ID NO:117)

MQVQIQSLFLLLLWVPGSRGFVEALFQEYNAAAKYLVIVFLINALACAGLAYKKFYFILVNLLKA
ALFFIIFNKNAAAKFVAAWTLKAAAKFILVNLLIFHNFQDEENIGIYKLPYGRTNLKAAAVLLGGV
GLVLNLIFFDLFLVKAVLAGLLGVV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGATTCGTGGAGGCCCTGTTTCAGGAATACAACGCCGCTGCAAAGTATCTCGTCATCGTGTTT
CTGATCAATGCTCTGGCATGCGCCGGCCTCGCTTACAAAAAGTTTTACTTCATTCTGGTCAACC
TGCTCAAGGCCGCTCTGTTCTTTATCATTTTCAATAAAAACGCCGCAGCTAAGTTTGTGGCCGC
ATGGACCCTGAAGGCCGCTGCAAAATTCATCCTCGTGAATCTGCTCATTTTTTCAAACTTCCAA
GACGAGGAAAATATCGGAATTTATAAGCTGCCCTACGGGAGGACAAACCTGAAAGCCGCTGC
AGTCTGCTCGGCCGAGTGGGGCTGGTGCTCAATTTTCTGATCTTCTTTGATCTGTTCTCTGGTG
AAGGCCGTCCTGGCCGGCCTGCTCGGAGTCGTGTGA (SEQ ID NO:118)

FIGURE 18H

PfCTL3 (SEQ ID NO:119)

MQVQIQSLFLLLLWVPGSRGVFLIFFDLFLNAAAPSDGKCNLYKAAAVTCGNGIQVRKLFHIFDGD
NEIKAHVLSHNSYEKNYYGKQENWYSLKKILSVFFLANAAAKFIKSLFHIFKAAALYISFYFIKAKF
VAAWTLKAAAKAAAYIPHQSSLKAAAGLIMVLSFL

ATGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA
GGAGTGTTCTGATCTTCTTTGACCTGTTCTGAAACGCCGCTGCACCCAGCGATGGCAAGTGC
AATCTCTACAAGGCCGCTGCAGTGACCTGTGGAACGGGATTAGGTGAGGAACTCTTTTCTCAC
ATCTTCGACGGCGATAACGAGATCAAGGCCCATGTGCTGTCCCAATTCTTATGAAAAAAC
TACTATGGAAGCAAGAGAATTGGTACAGCCTGAAGAAAATTCTGTCCGTGTTCTTTCTCGCC
AACGCCGCTGCAAAGTTTATCAAGTCTCTGTTCCATATTTTCAAGGCCGCTGCACTCTACATCA
GCTTCTATTTTATTAAAGCCAAATTTGTGGCCGCTTGACACTGAAGGCCGCTGCAAAGCCG
CTGCATACTATATCCCTCACCAGAGCTCCCTGAAGGCCGCTGCAGGGCTGATCATGGTGCTCT
CTTTCCTGTGA (SEQ ID NO:120)

PfCTL/HTL(N) (SEQ ID NO:121)

MQVQIQSLFLLLLWVPGSRGSSVFNVNSSIGLIMVLSFLGPGPGLYISFYFILVNLLIFHNGKIKN
SEGPGPGPDSIQDSLKESRKLSPGPGVLAGLLGVVSTVLLGGVGLVLPGPGLPSENERGYYPHQ
SSLGPGPGQTNFKSLRLNLGVSENIPLKGPFGQDEENIGIYGPBGKYLIVFLIFFDLFLVGP
GKFIKSLFHIFDGDNEIGPGPGKSKYKLATSVLAGLLGPGPLPYGKTNLGPGRHNWVNHAVPL
AMKLIGPGPMRKLAILSVSSFLFVEALFQEYGPBGVTCGNGIQVRGPGPMNYYGKQENWYSL
KKGPGPGPSDGKCNLYADSAWENVKNVIGPFMKAVCVEVGPBGKILSVFFLALFFIIFNKGP
HVLHNSYEKGPGPGKYKIAGGIAGGLALLACAGLAYKFVVPGAATPYAGEPAPF

ATGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA
GGAAGTAGTGTTCAATGTTGTGAACCTCATCAATTGGTCTGATCATGGTGCTGAGCTTTCTCG
GGCCAGGGCCAGGATTATATATTTCTTTCTACTTCATCCTTGTC AACCTGTTAATATTCCACAT
TAACGGCAAAATAATAAAGAACAGTGAAGGCCCTGGGCCTGGGCCTGACTCGATCCAGGATT
CTCTAAAAGAAATCGAGGAAGCTCTCCGACCAAGGCCCTGGTGTACTCGCCGGGTGCTGGGA
GTAGTTAGCACAGTGCTGTTAGGAGGCGTCGGCCTCGTCTTAGGACCTGGACCAGGTCTGCCG
TCCGAAAACGAAAGAGGATACTACATACCTCACCAGAGCAGCCTCGGCCAGGCCCGGACA
AACCAATTTCAAATCCCTCTTGCGAAATCTAGGAGTGAGCGAGAACATATTTCTTAAAGGACC
CGTCCCGGCTTTTCAAGGACGAGGAGAATATAGGTATTTACGGTCCAGGACCTGGAAAATACCT
AGTGATCGTATTCCTAATTTTTTTTGTACCTATTTCTGGTGGGCCAGGTCCCGGAAAGTTCATT
AAATCACTCTTCCACATTTTTTGTACGGAGATAACGAGATAGGACCCGGTCCCGGAAATCAA
GTACAAACTAGCCACTTCAGTGCTGGCCGGCCTTCTAGGGCCGGGCCAGGGCTCCCTATGG
AAAGACAAATCTTGCCCCGGTCCAGGACGGCACTGGGTGAATCATGCGGTTCATTGG
CCATGAAACTAATCGGGCCCGGTCCAGGCATGCGCAAACTTGCAATTCTAAGCGTAAGTTCAT
TTCTGTTTCGTAGAGGCACTGTTTCAAGAATATGGCCAGGACCTGGCGTCACATGTGGGAATG
GGATCCAGGTGAGAGGACCGGACCTGGTATGAACCTATTACGGTAAACAGGAAAATTGGTAC
TCCCTGAAAAAGGGTCCAGGCCCGGCCCTCAGATGGTAAGTGCAACCTGTATGCTGACTCA
GCATGGGAGAACGTAAAAAATGTAATAGGCCATTGTAAGGCAGTTTGTGTCGAAGTCGG
ACCAGGCCAGGAAAAATACTTTCTGTCTTCTTCTAGCTCTCTTCTTCATCATCTTCAACAAG
GGACCAGGCCAGGTACGTGTTATCCATAACTCTTATGAAAAAGGCCAGGACCTGGGAA
ATACAAAATCGCAGGAGGGATCGCCGGCGGGCTAGCGCTCCTTGCCCTGCGCAGGCTTGGCTTA
CAAATTCGTTGTACCAGGAGCTGCAACACCCTATGCAGGAGAACCTGCCCCATTTTGAAGATC
TGC (SEQ ID NO:122)

FIGURE 18I



PF33 (SEQ ID NO:123)

MGMQVQIQSLFLLLLWVPGSRGFMKAVCDEVNVTGNGIQVRKGLIMVLSFLNAALFHIFDGDN
EIKAAALLACAGLAYKKSFLFVEALFNAAPSDGKCNLYKAAQTNFKSLLRNLPSENERGYKAAAGVS
ENIFLNAAAAYFILVNLLIKAAAILSVSSFLFVNTPYAGEPAPFKAAAKYKLATSVLKAAVFLIFFDL
FLNYYIPHQSSLKAAGLLGNVSTVGAVLLGGVGLVNLACAGLAYKKAFIKSLFHIFKAAFYFIL
VNLLKAFLIFFDLFLVKALFFIIFNKNYYGKQENWYSLKFVEALFQEYNAAAKFVAAWTLKAAAK
ILSVFFLANAVLAGLLGNVNFQDEENIGIYKAAALYISFYFIKAFILVNLLIFHNAALPYGRTNLKAA
HVLSHNSYEKNAAAKYLVIVFLI

GCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCC
GGATCCAGAGGATTTATGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCGGTAACGGAAT
TCAGGTGAGAAAGGGACTCATCATGGTACTCAGCTTTCTGAACGCAGCCCTGTTCCACATCTT
TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGGACTAGCCTATAAAAAGA
GTTTCCTTTTCGTTGAAGCACTATTTAACGCAGCACCCAGTGACGGTAAATGCAACCTATATA
AAGCAGCTCAGACTAATTTCAAAGCCTGTAAAGAAATCTGCCCTCAGAGAATGAAAGGGGT
TACAAGCCCGCGCGTGTCCGAGAATATTTTCTGAAGAACGCCGCTGCTTATTTTATACTC
GTGAATCTACTCATAAAGGCAGCCGCAATCCTTTTCAGTGTCCAGCTTTCTGTTTGTAAACACAC
CATATGCGGGCGAGCCGGCTCCTTTCAAGGCTGCAGCAAAATACAAGCTTGCCACATCAGTAT
TGAAAGCAGCTGTGTTTTGATATTCTTTGATCTTTTTTAACTACTACATACCTCATCAGTCT
AGTCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCGCTTACTTGGAGGA
GTTGGCCTCGTGTGTAACCTCGCGTGCAGGTCTGGCCTACAAAAAAGCGAAATTCATCAAG
TCTCTGTTCCACATTTTTAAAGCCGCATTCTATTTCATACTAGTGAACCTTCTCAAAGCTTTCT
GATCTTCTTCGATCTATTCTCGTAAAAGCGCTATTCTTCATTATCTTTAACAAAAATTATTAC
GGCAAGCAAGAAAATTGGTACTCACTCAAGTTTGTAGAAGCTCTGTTCCAGGAATACAACGCC
GCTGCTAAATTGTTGCAGCTTGGACCTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTTC
TCGCTAATGCCGTATTAGCAGGACTTCTAGGCAACGTGAACTTTCAAGACGAAGAGAATATAG
GCATCTACAAAGCCGAGCACTGTACATTTTCTTACTTCAAGGCCTTCATACTGGTCAA
CCTTCTGATATTTCATAATGCAGCACTGCCATATGGGAGAACCAACTTGAAAGCGGCCCCACGT
GTTGAGCCACAACCTCTACGAGAAGAACGCCGCCGCGAAATATCTCGTCATTGTCTTCTGAT
TTGA (SEQ ID NO:124)

TB.1 (SEQ ID NO:125)

MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNLMIQTAAAVVKALVLLMLPVGA
GLMTAVYLVGAAAMALLRLPVKRMFAANLGVNSLYFGGICVGRPLVLPVAVNAAAACFVAAWT
LKAAAKAAARLMIGTAAAGFVVALIPLVNMATYAAPLFVGAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGATCCAGAGGAAGG
ATGAGCAGAGTGACCACATTCAGTCAAGGCCCTGGTGCTCCTGATGCTCCCCGTCGTGAAC
CTGATGATCGGCACCGCTGCAGCCGTCGTGAAAGCTCTCGTCCTGCTCATGCTCCCTGTGGGA
GCAGGGCTGATGACAGCCGTGTACCTGGTCGGCGCTGCAGCCATGGCCCTCCTGCGGCTGCCA
GTGAAGCGCATGTTTGCTGCAAATCTGGGAGTCAACTCCCTCTATTTGCGGGGCATTTGCGTG
GGAAGGCTGCCCTCGTGCTGCCTGCTGTGAATGCAGCCGCTGCCAAATTTGTCGCCGCTTGG
ACTCTGAAGGCAGCCGCTAAGGCCGCTGCAAGACTGATGATCGGGACCGCCGCTGCCGGCTT
CGTGGTCGCCCTGATTTCCCTGGTGAACGCCATGACATACGCAGCTCCTCTGTTTGTGGGAGC
CGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA (SEQ ID NO:126)

FIGURE 18J



BCL A2 #90 (SEQ ID NO:127)

MQVQIQSLFLLLLWVPGSRGIMIGHLVGVNRLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYL
SGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTRVNAAA
ATVGIMIGVNAKLCVPVQLWV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAATT
ATGATCGGCCATCTGGTGGGCGTCAACAGACTGCTGCAGGAAACCGAGCTGGTGAATGCCAA
GGTGGCCGAAATTGTGCACTTTCTCAACGCAAAGGTGTTTGGTTCCTGGCTTTTGTCAATGCC
TATCTGAGCGGCGCTAACCTCAACGTCGGAGCCGCTACCTCCAGCTGGTCTTCGGCATCGAG
GTCAACGCTGCTGCAAAATTCGTGGCAGCTTGGACCCTCAAGGCTGCAGCAAAGGCTGCCGCC
GTCGTGCTCGGAGTGGTGTTCGGGATCAACTCTATGCCACCTCCCGGGACTAGGGTCAATGCT
GCCGCCGCAACAGTGGGAATCATGATTGGGGTGAATGCCAACTGTGCCAGTGCAACTGTG
GGTGTGA (SEQ ID NO:128)

BCL A2 #88 (SEQ ID NO:129)

MQVQIQSLFLLLLWVPGSRGVVLGVVFGINAAAKFVAAWTLKAAAKVAEIVHFLNAYLSGANL
NVGAAYLQLVFGIEVNIMIGHLVGVNRLQETELVNAKVFGSLAFVNAKLCVPVQLWVNAAAATV
GIMIGVNSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAGTC
GTGCTGGGAGTCGTCTTCGGCATTAATGCCGCCGCTGCAAAGTTCGTGGCTGCCTGGACCCTG
AAGGCCGAGCTAAAGTGGCAGAGATCGTGCACTTTCTGAACGCCTACCTGAGCGGAGCAAA
TCTGAACGTCGGCGCTGCCTATCTGCAGCTCGTGTTTGAATTGAAGTGAACATCATGATTGG
ACATCTGGTGGGCGTGAACAGGCTGCTCCAGGAACTGAGCTGGTCAACGCTAAAGTGTTCG
GGTCTCTCGCCTTTGTGAACGCTAAGCTCTGCCCCGTCCAACCTCTGGGTCAATGCCGCAGCCG
CTACAGTGGGGATCATGATCGGCGTGAACCTCCATGCCTCCACCAGGGACCAGAGTGTGA

(SEQ ID NO:130)

BCL A2 #63 (SEQ ID NO:131)

MQVQIQSLFLLLLWVPGSRGKLCVPVQLWVNAAAATVGIMIGVNIMIGHLVGVNRLQETELVNA
KVAEIVHFLNAKVFGSLAFVNAYLSGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAA
AVVLGVVFGINSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAAAG
CTCTGCCCCGTGCAACTGTGGGTCAACGCCGCCGCCGCAACCGTCGGCATTATGATCGGGGTG
AACATCATGATCGGACACCTGGTCGGCGTGAACAGGCTGCTGCAGGAGACAGAACTGGTCAA
TGCCAAGGTGGCTGAAATTGTCCATTTCTGAATGCCAAAGTGTTCCGGCTCTCTCGCTTTCTGTG
AACGCTTATCTGAGCGGAGCTAACCTCAACGTGGGGGGCCGCATACCTCCAGCTCGTCTTTGGG
ATTGAGGTGAATGCCGCAGCTAAATTTGTGCTGCCTGGACCCTGAAGGCAGCAGCCAAGGCT
GCCGCAGTGGTGTGGGAGTGGTGTTCGAATCAATTCATGCCTCCACCAGGCACTAGAGTG
TGAGGATCC (SEQ ID NO:132)

FIGURE 18K



Prostate 1 (SEQ ID NO:133)

LTFFWLDRSVKAAAVLVHPQWVLT VKAAALLQERGVA YIKAALLSIALSVNPLVCNGVLQGVK
AAIMYSAHDTTVKAAAF LTPKKLQCVNAMMNDQLMFLNAGLPSIPVHPV KAAALGTTTCYVGAAL
LLWQPIPVNFLRPRSLQCVKAFL TLSVTWIGVNALL YSLVHNLGAATLMSAMTNL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCTGTGGGTGCCCGGGTCCAGAGGATTG
ACATTTTTTTTGGCTGGATAGATCGGTAAAGGCTGCAGCCGTGCTTGTTCATCCCCAGTGGGTCT
TGACCGTAAAGGCTGCCGCGCTGCTACAAGAAAGAGGGGTCGCATACATCAAAGCTGCTCTC
CTCTTGAGTATTGCGCTAAGTGTAACCCGCTAGTTTGTAATGGGGTGTTACAAGGTGTGAAA
GCGGCGATTATGTACAGTGCCACGACACTACCGTAAAAGCAGCCGCTTTCCTGACCCCAAAA
AAACTCCAATGCGTGAACGCAATGATGAATGATCAGCTGATGTTTTTAAACGCTGGCTTACCT
TCTATACCGGTTTCATCCAGTCAAGGCCGCGGCAATTGGGTACGACGTGTTATGTTGGAGCAGCG
ATACTTCTTTGGCAGCCCATACAGTAAATTTTTTAAGACCTAGATCCTTACAATGCGTCAAAG
CATTCTTACACTCTCAGTAACTTGGATCGGAGTCAATGCTCTGCTATATAGCCTCGTACACAA
CTTGGGCGCGGCCACACTTATGAGTGCAATGACGAATTTAGCTAAGTTTCGTGGCGGCCTGGAC
TCTAAAGGCCGCAGCA (SEQ ID NO:134)

HIV-1043 (SEQ ID NO:135)

MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGP GPGWFEVNTPLVKLWYQGP GPGYR
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGP GPGGEIYKRWILGLNKIVRMYGPGPGQGQM
VHQAI SPRTLNGPGPGIKQFINMWQEVGKAMYGPGPGWAGIKQEFIPYNPQGP GPGKTA VQMA
VFIHNFKRGP GPGSPAIFQSSMTKILEP GPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPP
GPGPGAETFYVDGAANRET KGP GPGGA VVIQD NSDIKVP GPGPGFRKYTAFTIPSINNE

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCCGGACC
TGGGCAGAAACAGATCACCAAGATCCAGA ACTTCCGGGTATACTACCGGGGACCTGGTCCAG
GTTGGGAGTTTGTGAACACACCACCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGAT
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCCGGGCCAGGCCAG
CACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAGCTGCAGGGGCCGGGCCCGGGGGGA
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGGCCAG
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG
GATGGGCAGGGATAAAACAGGAGTTTGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGT
AAAACGGCAGTGCAGATGGCCGTGTTCAATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGC
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCGGCCAGGGCCGGGCGAAGT
GAACATTGTACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAGGGCATTCCAA
TTGGCGGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAACTTT
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA
TTCAGGACAACTCAGACATCAAGGTGGTTCCTCGGTCCAGGCCCGGGTTCAGAAAGTATACCG
CCTTCACTATTCCGTCCATCAACAATGAGTGA (SEQ ID NO:136)

FIGURE 18L



HIV-1043 PADRE (SEQ ID NO:137)

MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGP GPGWFEVNTPLVKLWYQGP GPGYR
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGPGPGGEIYKRWILGLNKIVRMYGP GPGQGQM
VHQAI SPRTLNGPGPGIKQFINMWQEVGKAMYGP GPGWAGIKQEF GIPYNPQGPGPGKTA VQMA
VFIHNFKRGP GPGSPAIFQSSMTKILEP GPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPP
GPGPGAETFYVDGAANRETKGPGPGGA VVIQDNSDIKVP GPGPGFRKYTAFTIPSINNEGPGPGA
KFVAAWTLKAAA

ATGGAGAAGGTGTACCTGGCCTGGGTTCAGCCACAAAGGCATCGGGGGAGGGCCCCGGACC
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG
GTTGGGAGTTTGTGAACACACCACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCCGAT
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCCGGGCCAGGCCAG
CACCTTCTGCAGCTTACAGTGTGGGGAATTAACAGCTGCAGGGGCCGGGCCCGGGGGGGA
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGGCCAG
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG
GATGGGCAGGGATAAAACAGGAGTTTGAATCCCTTACAATCCCCAGGGTCTCTGGGCCAGGT
AAAACGGCAGTGCAGATGGCCGTGTTCAATCATAATTTAAGCGGGGCCCTGGACCTGGCAGC
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCGGCCAGGGCCGGGCGAAGT
GAACATTGTACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAGGGCATTCCAA
TTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAAACTTT
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA
TTCAGGACAACCTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCGGGTTCAGAAAGTATACCG
CCTTCACTATTCCGTCCATCAACAATGAGGGCCCCGGCCAGGTGCCAAGTTCGTGGCTGCCT
GGACCCTGAAGGCTGCCGCTTGA (SEQ ID NO:138)

HIV 75mer (SEQ ID NO:139)

EKVYLAWVPAHKGIGGGPGPGQGQM VHQAI SPRTLNGPGPGSPAIFQSSMTKILEP GPGPGFRKYTA
FTIPSINNE

GAGAAGGTGTACCTGGCCTGGGTGCCTGCCACAAAGGAATCGGAGGACCTGGCCCTGGACA
GGGACAGATGGTGCACAGGCCATCAGCCCTAGGACCCTGAACGGACCTGGACCTGGAAGCC
CTGCCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCGGACCTGGACCTGGATTAGGA
AGTACACCGCCTTACCATCCCCAGCATCAACAACGAGTGA (SEQ ID NO:140)

FIGURE 18M



PHITL (SEQ ID NO:141)

MQVQIQSLFLLLLWVPGSRGRHNWVNHAVPLAMKLIGPGPGKCNLYADSAWENVKNGPGPGKS
KYKLATSVLAGLLGPGPGQTNFKSLLRN LGVSEGPGPGSSVFN VVNSSIGLIMGPGPGVKNVIGPF
MKA VCVGPGPGMNYYGKQENWYSLKKGPGPGGLAYKFVVPGAATPYGPGPGPDSIQDSLKESR
KLNGPGPGLLIFHINGKIIKNSEGP GPGAGLLGNVSTVLLGGVGP GPGKYKIAGGIAGGLALLGPGP
GMRKLAILSVSSFLFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA
GGAAGGCACAACTGGGTGAATCATGCTGTGCCCTGGCTATGAAGCTGATCGGCCCTGGACC
AGGGAAATGCAACCTCTACGCAGACAGCGCCTGGGAGAACGTCAAGAATGGCCCCGGACCTG
GGAAATCCAAGTATAAGCTCGCTACCTCTGTGCTGGCAGGCCTGCTCGGACCAGGCCCGGAC
AGACAAATTTCAAAAGCCTGCTCAGAAACCTGGGAGTGTCCGAGGGGCCTGGCCCAGGATCT
AGCGTCTTTAATGTGGTCAACTCCTCTATTGGGCTCATCATGGGACCCGGACCTGGGGTGAAA
AATGTGATTGGCCCATTCATGAAGGCCGTGTGTGTGCGAAGGACCCGGGCCTGGCATGAACTAC
TATGGAAAGCAAGAAAATTGGTACAGCCTGAAGAAAGGCCCTGGGCCAGGCGGACTGGCTTA
CAAGTTTGTGGTCCCAGGGGCAGCCACTCCCTATGGGCCTGGGCCAGGCCCCGATTCCATCCA
GGACTCTCTCAAAGAGAGCCGGAAGTGAACGGACCCGGGCCTGGACTGCTCATTTTCCACAT
CAATGGCAAAATTATCAAGAACAGCGAGGGACCTGGGCCAGGCGCCGACTGCTGGGGAACG
TGTCACCGTCCTGCTCGGCGGAGTGGGGCCCCGGCCCTGGGAAGTACAAGATCGCTGGAGGG
ATCGCAGGCGGACTGGCCCTCCTGGGCCAGGACCAGGGATGCGCAAAGTGGCTATTCTCTCT
GTCTCCAGCTTTCTGTTTGTGTGA (SEQ ID NO:142)

FIGURE 18N



Protein	Sequence(SEQ ID NOS:143-340)	Restriction
HIV gag 386	VLAEAMSQV	HLA-A2
HIV gag 271	MTNNPPIPV	HLA-A2
HIV pol 774	MASDFNLPPV	HLA-A2
HIV pol 448	KLVGKLNWA	HLA-A2
HIV pol 163	LVGPTPVNI	HLA-A2
HIV pol 498	ILKEPVHGV	HLA-A2
HIV pol 879	KAACWWAGI	HLA-A2
HIV pol 132	KMIGGIGGFI	HLA-A2
HIV pol 772	RAMASDFNL	HLA-A2
HIV pol 183	TLNFPISPI	HLA-A2
HIV env 134	KLTPLCVTL	HLA-A2
HIV env 651	LLQLTVWGI	HLA-A2
HIV env 163	SLLNATDIAV	HLA-A2
HIV nef 221	LTFGWCFKL	HLA-A2
HIV vpr 59	AIIRILQQL	HLA-A2
HIV vpr 62	RILQQLLFI	HLA-A2
HIV pol 929	QMAVFIHNFK	HLA-A3
HIV pol 722	KVYLAWVPAHK	HLA-A3
HIV pol 971	KIQNFRVYYR	HLA-A3
HIV pol 347	AIFQSSMTK	HLA-A3
HIV pol 98	VTIKIGGQLK	HLA-A3
HIV env 61	TTLFCASDAK	HLA-A3
HIV env 47	VTVYYGVPVWK	HLA-A3
HIV nef 100	QVPLRPMTYK	HLA-A3
HIV vif 7	VMIVWQVDR	HLA-A3
HIV gag 162	QMVHQAISPR	HLA-A3
HIV gag 545	YPLASLRSLF	HLA-B7
HIV gag 237	HPVHAGPIA	HLA-B7
HIV pol 186	FPISPIETV	HLA-B7
HIV pol 893	IPYNPQSQGVV	HLA-B7
HIV env 259	IPIHYPAPA	HLA-B7
HIV env 250	CPKVSFEPI	HLA-B7
HIV nef 94	FPVRPQVPL	HLA-B7
HIV rev 75	VPLQLPPL	HLA-B7
HIV pol 684	EVNIVTDSQY	HLA-A1
HIV gag 317	FRDYVDRFY	HLA-A1
HIV pol 368	VYQYMDDL	HLA-A1
HIV pol 295	VTVLDVGDAY	HLA-A1
HIV pol 533	IYQEPFKNL	HLA-A24
HIV pol 244	PYNTPVFAI	HLA-A24
HIV pol 530	TYQIQEPF	HLA-A24
HIV pol 597	YWQATWIPEW	HLA-A24
HIV env 681	IWGCSGKLI	HLA-A24
HIV env 671	RYLKDQQLL	HLA-A24

FIGURE 19A



Protein	Sequence	Restriction
HIV env 55	VWKEATTTLF	HLA-A24
HIV vpr 46	IYETYGDTW	HLA-A24
HIV vpr 14	PYNEWTLEL	HLA-A24
HIV gag 298	KRWIILGLNKIVRMV	HLA-DR
HIV pol 596	WEFVNTPLVLKLYWYQ	HLA-DR
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR
HIV env 729	QHLLQLTVWGKQLQ	HLA-DR
HIV gag 171	QGQMVHQAIPTLN	HLA-DR
HIV pol 335	SPAIFQSSMTKILEP	HLA-DR
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR
HIV pol 758	HSNWRAMASDFNLPP	HLA-DR
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR
HIV vpr 31	YRKILRQRKIDRLID	HLA-DR3
HIV pol 874	WAGIKQEFGIPYNPQ	HLA-DR3
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3
HIV pol 619	AETFYVDGAANRETK	HLA-DR3
HIV pol 989	GAVVIQDNNDIKVVP	HLA-DR3
HCV NS4 1812	LLFNILGGWV	HLA-A2
HCV NS1/E2 728	FLLLADARV	HLA-A2
HCV NS4 1590	YLVAYQATV	HLA-A2
HCV NS5 2611	RLIVFPDLGV	HLA-A2
HCV CORE 132	DLMGYIPLV	HLA-A2
HCV NS4 1920	WMNRLIAFA	HLA-A2
HCV NS4 1666	VLVGGVLAA	HLA-A2
HCV NS4 1769	HMWNFISGI	HLA-A2
HCV NS4 1851	ILAGYGAGV	HLA-A2
HCV CORE 35	YLLPRRGPR	HLA-A2
HCV NS1/E2 726	LLFLLADA	HLA-A2
HCV LORF 1131	YLVTRHADV	HLA-A2
HCV CORE 51	KTSEERSQPR	HLA-A3
HCV CORE 43	RLGVRATRK	HLA-A3
HCV ENV1 290	QLFTFSPRR	HLA-A3
HCV NS1/E2 632	RMVVGGEVHR	HLA-A3
HCV NS3 1396	LIFCHSKKK	HLA-A3
HCV NS4 1863	GVAGALVAFK	HLA-A3
HCV NS4 1864	VAGALVAFK	HLA-A3
HCV NS3 1262	LGFGAYMSK	HLA-A3
HCV Core 169	LPGCSFSIF	HLA-B7
HCV NS5 2922	LSAFSLHSY	HLA-A1
HCV NS3 1128	CTCGSSDLY	HLA-A1
HCV NS5 2180	LTDPSHITA	HLA-A1

FIGURE 19B



Protein	Sequence	Restriction
HCV Core 126	LTCGFADLMGY	HLA-A1
HCV NS3 1305	LADGGCSGGAY	HLA-A1
HCV NS4 1765	FWAKHMWNF	HLA-A24
HCV NS5 2875	RMILMTHFF	HLA-A24
HCV NS5 2639	VMGSSYGF	HLA-A24
HCV NS4 1765	FWAKHMWNFI	HLA-A24
P. falciparum SSP2-230	FMKAVCVEV	HLA-A2
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2
P. falciparum CSP-7	ILSVSSFLFV	HLA-A2
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3
P. falciparum LSA1-105	GVSENIFLK	HLA-A3
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7
P. falciparum LSA1-1663	LPSENERGY	HLA-A1
P. falciparum EXP1-73	KYKLATSVL	HLA-A24
P. falciparum CSP-12	SFLFVEALF	HLA-A24
P. falciparum LSA1-10	YFILVNLLI	HLA-A24
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2
P. falciparum SSP2-523	LACAGLAYK	HLA-A3
P. falciparum EXP1-10	ALFFIIFNK	HLA-A3
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3
P. falciparum SSP2-126	LPYGRTNL	HLA-B7
P. falciparum CSP-15	FVEALFQEY	HLA-A1
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1
P. falciparum LSA1-9	FYFILVNLL	HLA-A24
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24
P. falciparum CSP-394	GLIMVLSFL	HLA-A2
P. falciparum EXP1-2	KILSVFFLA	HLA-A2
P. falciparum CSP-344	VTCGNGIQVR	HLA-A3
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24
P. falciparum LSA1-5	LYISFYFI	HLA-A24
P. falciparum CSP-2	MRKLAILSVSSFLFV	HLA-DR
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3

FIGURE 19C



Protein	Sequence	Restriction
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR
P. falciparum SSP2-527	GLAYKFVVPGAATPY	HLA-DR
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR
P. falciparum LSA1-16	LLIFHINGKIIKNS	HLA-DR
P. falciparum LSA1-94	QTNFKSLLRN LGVSE	HLA-DR
HBV core 18	FLPSDFFPSV	HLA-A2
HBV env 183	FLLTRILTI	HLA-A2
HBV env 335	WLSLLVPFV	HLA-A2
HBV pol 455	GLSRYVARL	HLA-A2
HBV pol 538	YMDDVVLGV	HLA-A2/A1
HBV pol 773	ILRGTSFVYV	HLA-A2
HBV pol 562	FLLSLGIHL	HLA-A2
HBV pol 642	ALMPYACI	HLA-A2
HBV env 338	GLSPTVWLSV	HLA-A2
HBV core 141	STLPETTVVRR	HLA-A3
HBV pol 149	HTLWKAGILYK	HLA-A3/A1
HBV pol 150	TLWKAGILYK	HLA-A3
HBV pol 388	LVVDFSQFSR	HLA-A3
HBV pol 47	NVSIPWTHK	HLA-A3
HBV pol 531	SAICSVVRR	HLA-A3
HBV pol 629	KVGNFTGLY	HLA-A3/A1
HBV pol 665	QAFTFSPTYK	HLA-A3
HBV core 19	LPSDFFPSV	HLA-B7
HBV env 313	IPIPSSWAF	HLA-B7
HBV pol 354	TPARVTGGVF	HLA-B7
TB	RMSRVTTFTV	HLA-A2
TB	ALVLLMLPVV	HLA-A2
TB	LMIGTAAAVV	HLA-A2
TB	ALVLLMLPV	HLA-A2
TB	GLMTAVYLV	HLA-A2
TB	MALLRLPV	HLA-A2
TB	RMFAANLGV	HLA-A2
TB	SLYFGGICV	HLA-A2
TB	RLPLVLPV	HLA-A2
TB	RLMIGTAA	HLA-A2
TB	FVVALIPLV	HLA-A2
TB	MTYAAPLFV	HLA-A2
TB	AMALLRLPLV	HLA-A2
p53 139	KLCPVQLWV	HLA-A2
CEA 687	ATVGIMIGV	HLA-A2
CEA 691	IMIGHLVGV	HLA-A2
Her2/neu 689	RLLQETELV	HLA-A2
MAGE3 112	KVAEIVHFL	HLA-A2

FIGURE 19D



Protein	Sequence	Restriction
Her2/neu 369	KVFGSLAFV	HLA-A2
CEA 605	YLSGANLNV	HLA-A2
MAGE2 157	YLQLVFGIEV	HLA-A2
Her2/neu 665	VVLGVVFGI	HLA-A2
p53 149	SMPPPGTRV	HLA-A2
PAP.21.T2	LTFFWLDRSV	HLA-A2
PAP.112	TLMSAMTNL	HLA-A2
PAP.284	IMYSAHDTTV	HLA-A2
PSM.288.V10	GLPSIPVHPV	HLA-A2
PSM.441	LLQERGVAYI	HLA-A2
PSM.469L2	LLYSLVHNL	HLA-A2
PSM.663	MMNDQLMFL	HLA-A2
PSA.3.V11	FLTLSVTWIGV	HLA-A2
PSA.143.V8	ALGTTCYV	HLA-A2
PSA.161	FLTPKKLQCV	HLA-A2
HuK2.4.L2	LLLSIALSV	HLA-A2
HuK2.53.V11	VLVHPQWVLTV	HLA-A2
HuK2.165	FLRPRSLQCV	HLA-A2
HuK2.216.V11	PLVCNGVLQGV	HLA-A2

FIGURE 19E